

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 20, 2004, 16:14:38 ; Search time 533 Seconds  
(without alignments)  
9764.571 Million cell updates/sec

Title: US-09-890-811B-9

Perfect score: 1928

Sequence: 1 gcacgagtcctcatctt.....tcaaaaaaaaaaaaaaaaaa 1928

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_19Jun03.\*  
1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.\*  
5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT.\*  
6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT.\*  
7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT.\*  
8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT.\*  
9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT.\*  
10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT.\*  
11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.\*  
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.\*  
13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.\*  
14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.\*  
15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.\*  
16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.\*  
17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT.\*  
18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.\*  
19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT.\*  
20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.\*  
21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.\*  
22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.\*  
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.\*  
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.\*  
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1928	100.0	1928	22	AAD09829 Soybean SPFI-relat
2	437.2	22.7	2008	24	ABX26660 Sunflower WRKY pol
3	355.8	18.5	373	25	ABX19178 Human GDP-mannose
4	342.2	17.7	421	25	ABX22865 Human GDP-mannose
5	312.6	16.2	363	25	ABX19862 Human GDP-mannose
6	308.2	16.0	1539	21	AAC43176 Arabidopsis thalia
7	308.2	16.0	1539	24	ABZ12999 Arabidopsis thalia
8	270.2	14.0	1182	24	ABZ13876 Arabidopsis thalia

9	259.2	13.4	1589	21	AAC40213 Arabidopsis thalia
10	256	13.3	265	25	ABX26660 Human GDP-mannose
11	232.8	12.1	2343	24	ABX59412 Soybean WRKY polyn
12	228.8	11.9	1542	24	ABZ12620 Arabidopsis thalia
13	228.8	11.9	1542	25	ABZ42035 Arabidopsis thalia
14	221.6	11.5	2158	22	AAD09830 Wheat SPFI-related
15	221.4	11.5	1545	22	ABZ14474 Arabidopsis thalia
16	221.4	11.5	1545	25	ABZ42023 Arabidopsis thalia
17	208.2	10.8	1626	24	AAI48565 A thaliana WRKY33
18	187.6	9.7	2086	22	AAD09828 Rice SPFI-related
19	177.8	9.2	1617	24	ABX59408 Sunflower WRKY pol
20	176.6	9.2	2603	24	ABK65157 Arabidopsis cDNA e
21	175.6	9.1	2208	24	ABX59420 Maize WRKY polynuc
22	175.4	9.1	378	21	AAC57119 Pinus radiata tran
23	167	8.7	2215	24	ABK65153 Arabidopsis cDNA e
24	166.4	8.6	1961	22	AAD09827 Rice SPFI-related
25	162.8	8.4	403	25	ABX62630 Arabidopsis thalia
26	161.6	8.4	835	24	ABN98908 Arabidopsis thalia
27	158	8.2	1179	24	ABX59416 Maize WRKY polynuc
28	154.6	8.0	930	21	AAC48843 Arabidopsis thalia
29	154.6	8.0	1065	21	AAC47116 Arabidopsis thalia
30	152.6	7.9	1538	24	ABX59406 Sunflower WRKY pol
31	147	7.6	1536	24	ABX59407 Sunflower WRKY pol
32	141.6	7.3	306	25	ABX85599 Corn ear-derived p
33	139.6	7.2	961	24	ABX59414 Wheat WRKY polynuc
34	130.2	6.8	2043	24	AAI48588 A thaliana WRKY33
35	119.4	6.2	1464	24	ABZ13768 Arabidopsis thalia
36	112.2	5.8	522	24	ABX59411 Soybean WRKY polyn
37	111.4	5.8	624	21	AAC38694 Arabidopsis thalia
38	109	5.7	1136	22	AAD05836 Arabidopsis thalia
39	109	5.7	1136	24	ABK65303 Arabidopsis cDNA e
40	108.2	5.6	444	21	AAC45051 Arabidopsis thalia
41	108.2	5.6	548	21	AAC35279 Arabidopsis thalia
42	108.2	5.6	569	21	AAC48380 Arabidopsis thalia
43	107	5.5	837	22	AAF80410 Nucleotide sequenc
44	107	5.5	837	24	ABK65175 Arabidopsis cDNA e
45	107	5.5	843	21	AAC37750 Arabidopsis thalia

## ALIGNMENTS

RESULT 1  
AAD09829  
ID AAD09829 standard; cDNA; 1928 BP.  
XX  
AC AAD09829;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Soybean SPFI-related transcription factor #5 cDNA.  
XX  
KW Soybean; SPFI-related transcription factor; transgenic plant;  
KW genetical mapping; physical mapping; plant breeding; ss.  
XX  
OS Glycine max.  
XX  
FH Key Location/Qualifiers  
FT CDS 12..1739  
FT /\*tag= a  
FT /product= "SPFI-related transcription factor #5"  
XX  
PN WO200149840-A2.  
XX  
PD 12-JUL-2001.  
XX  
PF 22-DEC-2000; 2000WO-US35310.  
XX  
PR 04-JAN-2000; 2000US-0174325.  
XX  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
PI Zhu Q, Famodu OO, Rafalski JA;

XX WPI: 2001-441876/47.  
 DR P-PSDB; AAE05092.  
 XX  
 PT Novel isolated SPF-1 related transcription factor polypeptides and  
 PT polynucleotides useful for producing transgenic plants -  
 XX  
 PS Claim 7; Page 52-53; 60pp; English.  
 XX  
 CC The present sequence is soybean SPFI-related transcription factor #5  
 CC cDNA. The SPFI-related transcription factor is useful for transforming a  
 CC cell by introducing SPFI-related transcription factor into a cell. It is  
 CC also useful for producing a transgenic plant by transforming a plant cell  
 CC with SPFI-related transcription factor and regenerating a plant from the  
 CC transformed plant cell. It is also useful to create transgenic plants in  
 CC which SPFI-related transcription factor DNA is present at higher or lower  
 CC levels than normal or in cell types or developmental stages in which they  
 CC are not normally found. The SPFI-related transcription factor DNA is  
 CC useful to prepare antibodies. It is also used as probes for genetically  
 CC and physically mapping the genes that they are a part of, and used as  
 CC markers for traits linked to these genes. Such information is useful in  
 CC plant breeding in order to develop lines with desired phenotype.  
 XX  
 SQ Sequence 1928 BP; 591 A; 454 C; 387 G; 496 T; 0 other;  
 Query Match 100.0%; Score 1928; DB 22; Length 1928;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1928; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCACGAGTCTCATGGCATCTTCTTCTGGTAGTTTACACACCTCTGCAAGTGCACCTCTCT 60  
 DB 1 GCACGAGTCTCATGGCATCTTCTTCTGGTAGTTTACACACCTCTGCAAGTGCACCTCTCT 60  
 QY 61 TCACCAACTTCACTTCTCCACACACCTTTCATGACCACTTCTTCTGACCTCTCTG 120  
 DB 61 TCACCAACTTCACTTCTCCACACACCTTTCATGACCACTTCTTCTGACCTCTCTG 120  
 QY 121 CTTCTCCCTTGGACACCAACGACCACTTCTGAGGTGTTGTCTGAGAGCACTTCTGCTC 180  
 DB 121 CTTCTCCCTTGGACACCAACGACCACTTCTGAGGTGTTGTCTGAGAGCACTTCTGCTC 180  
 QY 181 GTGTTCCCAATTCAGTCCACACCACTTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 240  
 DB 181 GTGTTCCCAATTCAGTCCACACCACTTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 240  
 QY 241 CTCCTTCTTCTTACTTGTCTATCTCTCTGTTGAGCCCTCTGCTGAGCTTCTTGA 300  
 DB 241 CTCCTTCTTCTTACTTGTCTATCTCTCTGTTGAGCCCTCTGCTGAGCTTCTTGA 300  
 QY 301 CGGTTCTCTTAACTCTTCCAACTTCTGCACTCTCCAACTGGAGCACTTGTGCTC 360  
 DB 301 CGGTTCTCTTAACTCTTCCAACTTCTGCACTCTCCAACTGGAGCACTTGTGCTC 360  
 QY 361 AGAGCTTCAATTCGAAGAGCAGTTCAGGGGGGAATCAGCAAAATGTCAAGAGAGAGACA 420  
 DB 361 AGAGCTTCAATTCGAAGAGCAGTTCAGGGGGGAATCAGCAAAATGTCAAGAGAGAGACA 420  
 QY 421 AAGGCTTCTCAAAATTTCTTTTCCAAACCCGATCAGGACCTCTCTGCTTCAATCAGCAA 480  
 DB 421 AAGGCTTCTCAAAATTTCTTTTCCAAACCCGATCAGGACCTCTCTGCTTCAATCAGCAA 480  
 QY 481 CATACCACTCTTCAAAATGTCCAGAGTTCACACCAACAGCCATGGATTTTTCAGGAGCCA 540  
 DB 481 CATACCACTCTTCAAAATGTCCAGAGTTCACACCAACAGCCATGGATTTTTCAGGAGCCA 540  
 QY 541 CGAAACAGGATTAATTTTCTTCCAGGAAGGGTATGATGAAATCTGAAAACTCTTCTTCCA 600  
 DB 541 CGAAACAGGATTAATTTTCTTCCAGGAAGGGTATGATGAAATCTGAAAACTCTTCTTCCA 600  
 QY 601 TGACAGATTTTCCCTTGAGATTTGCTAGTGTCCAAACTAAACATAGCAATGGGTTTCAAT 660  
 DB 601 TGACAGATTTTCCCTTGAGATTTGCTAGTGTCCAAACTAAACATAGCAATGGGTTTCAAT 660

QY 661 CCGATTATGGCAATTAACCCCCACCAATCTCAGACTTTTAAGTAGAAGGTGAGATGGGT 720  
 DB 661 CCGATTATGGCAATTAACCCCCACCAATCTCAGACTTTTAAGTAGAAGGTGAGATGGGT 720  
 QY 721 ACAATTTGAGGAAATATGCGCAAAACCAAGTGAAGGAGTGAATAATCAAGAAGTTATT 780  
 DB 721 ACAATTTGAGGAAATATGCGCAAAACCAAGTGAAGGAGTGAATAATCAAGAAGTTATT 780  
 QY 781 ACAATTTGAGGAAATATGCGCAAAACCAAGTGAAGGAGTGAATAATCAAGAAGTTATT 840  
 DB 781 ACAATTTGAGGAAATATGCGCAAAACCAAGTGAAGGAGTGAATAATCAAGAAGTTATT 840  
 QY 841 AAATTAAGTGAAGTGAATTAAGGAGTGAATTAAGGAGTGAATTAAGGAGTGAATTAAGGAG 900  
 DB 841 AAATTAAGTGAAGTGAATTAAGGAGTGAATTAAGGAGTGAATTAAGGAGTGAATTAAGGAG 900  
 QY 901 GAAATCTCAATCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960  
 DB 901 GAAATCTCAATCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960  
 QY 961 TCCAGATCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020  
 DB 961 TCCAGATCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020  
 QY 1021 AAAAATCTCAATCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080  
 DB 1021 AAAAATCTCAATCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1080  
 QY 1081 CAGGAGGGGATGAATATGATGAAGATGAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140  
 DB 1081 CAGGAGGGGATGAATATGATGAAGATGAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140  
 QY 1141 AAAATGAGGTATGTCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200  
 DB 1141 AAAATGAGGTATGTCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1200  
 QY 1201 AGACAACCACTGACATTTGATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1260  
 DB 1201 AGACAACCACTGACATTTGATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1260  
 QY 1261 AAGTAGTGAAGGGCAATCCAAATCCAAAGGAGTACTTCAAGTGCACACACCCAGGATGTC 1320  
 DB 1261 AAGTAGTGAAGGGCAATCCAAATCCAAAGGAGTACTTCAAGTGCACACACCCAGGATGTC 1320  
 QY 1321 CAGTGAAGGAGCAGCTGGAAGAGGCTCAGATGAGGCTGATGAGGCTGATGAGGCTGATGAG 1380  
 DB 1321 CAGTGAAGGAGCAGCTGGAAGAGGCTCAGATGAGGCTGATGAGGCTGATGAGGCTGATGAG 1380  
 QY 1381 AGGGAAGCACAACCACTGATGTTCTCTGACCCCTGCGAGTGGCAGCCATTTCTGTGAACA 1440  
 DB 1381 AGGGAAGCACAACCACTGATGTTCTCTGACCCCTGCGAGTGGCAGCCATTTCTGTGAACA 1440  
 QY 1441 GACCAATGCAAAACCAATGTTCAAAACCAACCACTGAGGCTCTCTGAGGCTCTCT 1500  
 DB 1441 GACCAATGCAAAACCAATGTTCAAAACCAACCACTGAGGCTCTCTGAGGCTCTCT 1500  
 QY 1501 TGCCAGTGAATCCCAAAAGTGAATTTCCCTTTCAGAACCAAGATCAGACACCAACCCAG 1560  
 DB 1501 TGCCAGTGAATCCCAAAAGTGAATTTCCCTTTCAGAACCAAGATCAGACACCAACCCAG 1560  
 QY 1561 AAGGGAATCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1620  
 DB 1561 AAGGGAATCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1620  
 QY 1621 GGTGTTGGGAATCAATGCAATCTTACGTGAACAGCAGCAACTATCTGCAATGTTTCTCT 1680  
 DB 1621 GGTGTTGGGAATCAATGCAATCTTACGTGAACAGCAGCAACTATCTGCAATGTTTCTCT 1680  
 QY 1681 CCTCCAGGACCAAGGAGGAGCTAGAGTGAATGTCCTCTCTCTCTCTCTCTCTCTCTCTCT 1740  
 DB 1681 CCTCCAGGACCAAGGAGGAGCTAGAGTGAATGTCCTCTCTCTCTCTCTCTCTCTCTCTCT 1740  
 QY 1741 GGAATTTTTTTTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1800

Db 1741 GGAATTTTTCCTTTTTCCTAGCTATGGAAGGTTGGAAATTTTGGAAAGTGGGGA 1800  
QY 1801 CTAGGATTTTATTCGACAAATAAGGTTCCATTTCGATTTATTTGGTTTGGTTTGG 1860  
Db 1801 CTAGGATTTTATTCGACAAATAAGGTTCCATTTCGATTTATTTGGTTTGGTTTGG 1860  
QY 1861 TTGTAAATTTTATACAGCCACAGGATTTGGTATAGTATATATCTAGTATTTCAAAAAA 1920  
Db 1861 TTGTAAATTTTATACAGCCACAGGATTTGGTATAGTATATATCTAGTATTTCAAAAAA 1920  
QY 1921 AAAAAAAA 1928  
Db 1921 AAAAAAAA 1928

RESULT 2  
ID ABS59405 standard; cDNA; 2008 BP.  
XX AC ABS59405;  
XX DT 05-NOV-2002 (first entry)  
XX DE Sunflower WRKY polynucleotide #1.  
XX KW WRKY; gene; ss; plant; zinc-finger-type factor; WRKY; SAR; sunflower;  
KW SA-dependent structure-activity analysis response; pathogen resistance;  
KW maize; wheat; rice; soybean.  
XX OS Helianthus annuus.  
XX PN US2002076775-A1.  
XX PD 20-JUN-2002.  
XX PF 16-MAR-2001; 2001US-0810264.  
XX PR 17-MAR-2000; 2000US-190467P.  
XX PA (CRAN/) CRANE V C.  
PA (FAMO/) FAMODU O.  
PA (HUXX/) HU X.  
PA (LUGG/) LU G.  
PA (ZHAN/) ZHANG L.  
XX PI Crane VC, Famodu O, Hu X, Lu G, Zhang L;  
XX WPI; 2002-582922/62.  
XX P-PSDB; ABG76909.  
XX PT New isolated plant-specific zinc-finger-type factor polynucleotide,  
XX useful for e.g. regulating the SA-dependent structure-activity analysis  
XX response in a plant -  
XX Claim 21; Page 32-34; 66pp; English.  
XX The invention relates to an isolated polynucleotide encoding a  
XX plant-specific zinc-finger-type factor (WRKY) protein. The DNA and  
XX protein are used to modulate the level of a WRKY protein in a plant and  
XX to regulate the SA-dependent structure-activity analysis (SAR) response  
XX in a plant. The sequences can be used to engineer plants to resist  
XX pathogens such as viruses, bacteria, insects and fungi, and to survive  
XX stress. They may also be used as a molecular probe to track inheritance  
XX of corresponding loci in genetic crosses and facilitate the plant  
XX breeding process, to isolate, identify and genetically map WRKY and other  
XX closely related disease resistance genes and to find genes and their  
XX promoters that respond to a WRKY domain. This sequence represents DNA  
XX encoding a WRKY polypeptide of the invention.  
XX SQ .Sequence 2008 BP; 616 A; 463 C; 388 G; 541 T; 0 other;  
Query Match 22.7%; Score 437.2; DB 24; Length 2008;

Best Local Similarity 57.4%; Pred. No. 5.3e-104;  
Matches 1000; Conservative 0; Mismatches 673; Indels 69; Gaps 9;  
QY 17 ATCTCTCTCTGTAGTTTGTAGACACCTCTGCAAGTGCACAACTCTTCCACCACTTCAACCTT 76  
Db 23 ATCTCTCTCTATAATAGATTTTTCATCTCTCTCAGGTATCACCTTGAACACCACTTC 82  
QY 77 TCTCCACACACCTTTTCATGACCACTTTCTTCTCTGACCTCTTGTCTTCTCTCTCTGACAA 136  
Db 83 TCTCCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 142  
QY 137 CAACAGCCACACAGGTTGTTGTCTGAGAGAACTGGCTCTGTGTCTGTCTGTCTGTCTGTCT 196  
Db 143 AACCAACCGGACTCGCTGCGCGGATCGCGAACGAGTCGGCTCGGTATTTCCAAAGTTCAA 202  
QY 197 GTCCACACACCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 256  
Db 203 GTCAATCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 262  
QY 257 TGTATTTCTCTGTGTTTGTAGCCCTGTGAGCTTTCTGACTCGCGGTTCTCTTAACTC 316  
Db 263 TGTATTTCTCTGTGTTTGTAGCCCTGTGAGCTTTCTGACTCGCGGTTCTCTTAACTC 322  
QY 317 TTCCAACTTTCTGCTATCTCCAACTTCCAACTTCCAACTTCCAACTTCCAACTTCCAACT 376  
Db 323 TTCCAACTTTCTGCTATCTCCGCTCTCGACTACCGGTTCTTCCCACTTTCAAGCTTTTAACT 382  
QY 377 GA-----CGAGTTTCAGGGGGGAATCAGCAAAATTTGTCAAGGAGAAAGACAAAAGCTT 427  
Db 383 GAATCTGAACGGCAACTTCCATAATGAAGAACTAGCATCAAAAGGAGCAAAAAGCTT 442  
QY 428 CTCAAAATTTCTCTTTTCCAAACCGGATCAGGACTCTCTGCTTCTCATCCACAGCAACATACCA 487  
Db 443 GCGGATTTCTCTTTTTCGACCACT-----TGATCATCTCTACGGAGCAACAGATAT 495  
QY 488 GTCTTCAAATGTCAAGTTCAAACACACAGCCATGGAGTTTTCAGGAGGCCACGAAACA 547  
Db 496 GGAATAATCAGAAACACAGATAGATCAGACGAAATCTTTTAAACCAATCGGACACT 555  
QY 548 GGATAATTTTCTCTCAGGAAAGGGTATGATGAAACTGAAACTCTTCTCTCATGCGAG 607  
Db 556 CGCC-----TCCGATGACAGCTTCTACCCGAAATCGCAAACTTCAAC----- 601  
QY 608 TTTTTCCTCTGAGATTGCTAGTGTCCAACTAACCATAGCAATGGGTTTCAATCCGATTA 667  
Db 602 -----CGATTCAAACCTCACAGCACAAAGCTTCCAACTCTGTT-ATGACACCAA 649  
QY 668 TGGCAATTACCCCTCCCAATCTCAGACTTTTAAGTAGAGGTGAGGTGAGGTGAGGTGAGGTG 727  
Db 650 CAGCAGCAGCAACTTCAACCAACCAACCGTTACAGAAAGTTCAGAAAGCGGTTATAATTG 709  
QY 728 GAGGAATATGCGCAAAACAACTGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 787  
Db 710 GCGAAATATCAGGGGCAAAACAAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 769  
QY 788 CACATACCCCAATTCCTCTTCTGCAATCCCTCATTCATTCATTCATTCATTCATTCATTCAT 847  
Db 770 CAGGTATCAAATTTGTCTCAATGAAGAGAACTAGAGACTATATAGAGGACAGATTAC 829  
QY 848 TGAGATAGTTTATAGGGTACTCATAAACCATCTTAAGCTCTAAATATCTAGGAGAACTC 907  
Db 830 TGAGATAGTTTATAGGGTAAATCATATAATCACCGGAAACCGCAATCTTACCGAAGATCATC 889  
QY 908 ATCAAACTCTCTCTCTGCAATCCCTCATTCATTCATTCATTCATTCATTCATTCATTCAT 955  
Db 890 GTCTTCTCTGCGGTTCTGAATCTTTGAGATGAGTCAAGGCTTCAAGTAATCATGATGTCA 949  
QY 956 TGAATATCCAGATCAATCTATGCGACACATCGAAGTGGAGCAAAATGGATTTCAGCTGCCAC 1015  
Db 950 TGAATATCCCGGATCAGTCTTATGTTTCTCATGAGTCCGGGAGGTTGATTCGGTTACTAC 1009  
QY 1016 CCCAGAAAACTCATCAATATCAATTTGGAGATGATGATTTTGGAGCAGAGTTCCTCAAAAGTG 1075

Db	1010	GCCGGAAAAATTCCTTCGATTTCCGGTCGGAGATGATGAGTTCGATTCGGAGT-----AGGTC	1063
Qy	1076	TAAATCAGGAGGGGATGAATATATGATGAAGATGAACCTGATGCCAAAAGATGGAAAAATTGA	1135
Db	1064	CGGTGGGATGGTGTACTGTTGATGAAGATGAGCCTGAGGCCAAAAGATGGAAGGTGTC	1123
Qy	1136	AGGTGAAAAATGAGGGTATGTCAGCCCTGGAAAGTAGAAACAGTAGTGAGAAACCTTAGATTGT	1195
Db	1124	GGAAAAATGAAGGGATATCAATGATTGGTGGAAACAAAGACGGTACGAAACCGAGGATCGT	1183
Qy	1196	AGTTTCAGACAAACAGTCACATTCGATTCCTTGTATGATGGCTATATAGGTGGAGAAAAATACGG	1255
Db	1184	GGTTCAAACAGCACCGCATATTGATATCTCGATGATGGTTATAGATGGAGAAAAATACGG	1243
Qy	1256	GCAGAAATGATGTAAGGGCAATCCAAATCCAAAGGAGTTACTTACAAGTGCACACACCCAGG	1315
Db	1244	TCAAAAGTGGTCAAGGGAAACCCAAATCCAAAGGAGTTATTACAAATGCACAACTTAGG	1303
Qy	1316	ATGTCCAGTGAGGAAGCAGCTGGAAAGAGCCTCAATGACCTTAAGGGCTGTGATCACAAC	1375
Db	1304	TTGTTCTGTAAAGAAAAATGTGGAGCCGAGCGTCAAAAGACTTGAGGTTCAGTAAATAACGAC	1363
Qy	1376	TTATGAGGGAAAGCACACCAATGATGTTCTTCGAGCCCGTGGCAGTGCAGGCCAATTCCTGT	1435
Db	1364	CTACGAGGGAAACACAAACCAATGATGTCCCAATGCTCTGGGGCTCG---GCCATCGGTT	1420
Qy	1436	GAACAGACCCAATGCCAAACAATGCTTCAAACACCAACCAACACTGACGCCACTTCCGTAAG	1495
Db	1421	ACRAGCTTCAACCCCTAAGCAACAATCGCCCTCGATGACAAATTAACCTATGGCACTATC	1480
Qy	1496	GCTCTTGCAGTGATCCACCAAAGTGACAAATTCCTTCAGNAACCAAGATCAAGACACC	1555
Db	1481	TCATPATCAAGTTGACAACTCCATGGTGGATCCAACTCGTGGCCGAGGTACCCCTCCCTC	1540
Qy	1556	ACCAGAAGGGCAATCACCCCTTCAACCCTAGAGATGCTACAAAGTCCAGGAAGTTTGGATT	1615
Db	1541	ATCTGAAAAATCAAGCACCTTTAGTTGGAGATGTTACAAAGTCTCATTAATTTAAGTA	1600
Qy	1616	CTCAGGTTTGGGAATCCAATGCAATCTTACGTGAACACGACGACAACTATCTGCAATGT	1675
Db	1601	TTCCAGATTTGAGAAATGCAATGAAAGTCCAAATATAATGAAACATAAATTCAGAAAGACGTT	1660
Qy	1676	TTTTCTCTCCAGGACCAAGGAGGAGCCTAGAGATGACATGTTCCCTTCAGGTCTCTACTATG	1735
Db	1661	T-----TCTACGACTAAAGAAGAACCTAGAGATGACATGTTCTTTGAGTCATTACTCTT	1714
Qy	1736	CT 1737	
Db	1715	CT 1716	
RESULT 3			
ABX19178			
ID	ABX19178 standard; cDNA; 373 bp.		
XX			
AC	ABX19178;		
XX			
DT	10-FEB-2003 (first entry)		
XX			
DE	Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #1235.		

XX	11-JUN-2001; 2001US-0878574.
XX	
XX	22-NOV-1996; 96US-0753233.
PR	03-DEC-1997; 97US-0984246.
PR	09-SEP-1998; 98US-0149674.
PR	14-JUN-1999; 99US-0333177.
XX	(GEMY ) GENETICS INST INC.
XX	Sullivan F, Kriz R, Kumar R;
PI	
XX	WPI; 2003-066673/06.
DR	
XX	New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D)
PT	peptide, for manufacturing complex carbohydrates, or as targets for
PT	screening GM4,6D antagonists for treating e.g. arthritis, or transplant
PT	rejection -
XX	
XX	Disclosure; SEQ ID NO 1237; 6pp; English.
XX	
XX	The invention relates to a composition comprising a human GDP-mannose
CC	4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying
CC	GM4,6D inhibitors. GM4,6D inhibitors are useful for reducing inflammation
CC	in a mammalian subject and for treating or ameliorating diseases affected
CC	by the level of cellular fucosylation or diseases affected by the
CC	fucosylation of glycoconjugates. These diseases include arthritis,
CC	transplant rejection, asthma, sepsis, reperfusion injury, stroke or
CC	infection. The GM4,6D peptide or a polynucleotide encoding it is also
CC	useful for manufacturing complex carbohydrates and as targets for
CC	screening small molecule antagonists of the activity of the enzyme. The
CC	polynucleotide is useful in developing an assay for defects in the
CC	enzyme, as well as in gene replacement therapy. Sequences
CC	ABX17942-ABX17944 and ABX17947-ABX33716 represent DNA molecules encoding
CC	human GM4,6D peptides of the invention.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification but was obtained in electronic format directly from USPTO
CC	at seqdata.uspto.gov/sequence.html.
XX	
XX	Sequence 373 BP; 67 A; 131 C; 56 G; 119 T; 0 other;
QQ	
Query Match	18.5%; Score 355.8; DB 25; Length 373;
Best Local Similarity	99.4%; Pred. No. 5.1e-83;
Matches	357; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	1 GCACGAGTCTCATGGCATTCTTCTTGTTAGTTTAGCACCTCTGCAAGTGCAAACCTCT 60
Dd	15 GCTCGAGTCTCATGGCATTCTTCTTGTTAGTTTAGCACCTCTGCAAGTGCAAACCTCT 74
Qy	61 TCACCACACTTCACCTTCTCCACACACCTTTCATGACCACTTCTTCTCGACCTCCCTTG 120
Dd	75 TCACCAACTTCACTTCTCCACACACCTTTCATGACCACTTCTTCTCGACCTCCCTTG 134
Qy	121 CTTCCTCCCTTGGACAACAACAGCCACCACAGGGTGGTTTTGTCTGAGAGAATGGGCTGTG 180
Dd	135 CTTCCTCCCTTGGACAACAACAGCCACCACAGGGTGGTTTTGTCTGAGAGAATGGGCTGTG 194
Qy	181 GTGTTCCCAAAATTAAGTCCACACACCACTTCTCTGCCTCTCTCTCCGCCCTCCCAATTT 240
Dd	195 GTGTTCCCAAAATTAAGTCCACACCACTTCTCTGCCTCTCTCTCCGCCCTCCCAATTT 254
Qy	241 CTCCTTCTCTTACTTTGCTATTCTCTCTGTTTGGCCCTGCTGAGCTTCTTTCGACTCGC 300
Dd	255 CTCCTTCTCTTACTTTGCTATTCTCTCTGTTTGGCCCTGCTGAGCTTCTTTCGACTCGC 314
Qy	301 CGGTTCTCTTAACTTCTCCAACATTTCTGCCATCTCCAACAACCTGGAGCAATTTGTTGCT 359
Dd	315 CGGTTCTCTTAACTTCTCCAACATTTCTGCCATCTCCAACAACCTGGAGCAATTTGTTGCT 373
RESULT 4	
ABX22865	
ID	ABX22865 standard; cDNA: 421 BP.



CC polynucleotide is useful in developing an assay for defects in the  
 CC enzyme, as well as in gene replacement therapy. Sequences  
 CC ABX17942-ABX17944 and ABX17947-ABX33716 represent DNA molecules encoding  
 CC human GM4,6D peptides of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format directly from USPTO  
 CC at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
 XX  
 SQ Sequence 363 BP; 67 A; 128 C; 52 G; 116 T; 0 other;

Query Match 16.2%; Score 312.6; DB 25; Length 363;  
 Best Local Similarity 93.7%; Pred. No. 1e-71;  
 Matches 340; Conservative 0; Mismatches 14; Indels 9; Gaps 1;

QY 15 GCATCTCTCTGTTAGACACCTCTGCAAGTGCACAACTCCTTCACCAACTTCACC 74  
 |||||  
 DB 1 GCATCTCTCTGTTAGACACCTCTGCAAGTGCACAACTCCTTCACCAACTTCACC 60  
 |||||

QY 75 TTCTCCACACACCTTTTCATGACACCTTTCTCTGACCTCTCTGCTTCTCCCTTGGAC 134  
 |||||  
 DB 61 TTCTCCACACACCTTTTCATGACACCTTTCTCTGACCTTTCTGCTTCTCCACAGAC 120  
 |||||

QY 135 AACCAAGCCACACACA-----GGTGGTTTGTCTGAGAGAACTGGCTCTGGTGT 185  
 |||||  
 DB 121 AACCAAGCCACACACATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 180  
 |||||

QY 186 CCNAATTCAGTCCACACACACACCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 245  
 |||||  
 DB 181 CCNAATTCAGTCCACACACACACCTTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240  
 |||||

QY 246 TCTCTTACTTTTGTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 305  
 |||||  
 DB 241 TCTCTTACTTTTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300  
 |||||

QY 306 CTCCTTAACCTTCCCAACATTTGCTCCATCTCCCAACCTGAGCATTTGTTGCTCAGAGC 365  
 |||||  
 DB 301 CTCCTTAACCTTCCCAAGATTTGCTCCATCTCCCAACCTGAGCATTTGTTGCTCAGAGC 360  
 |||||

QY 366 TTC 368  
 |||||  
 DB 361 TTC 363

RESULT 6  
 AAC43176  
 ID AAC43176 standard; DNA; 1539 BP.  
 XX  
 AC AAC43176;  
 XX  
 DT 17-OCT-2000 (first entry)  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38308.  
 XX  
 KW Hybridisation assay; genetic mapping; gene expression control;  
 KW protein identification; signal transduction pathway;  
 KW metabolic pathway; promoter; termination sequence; ss.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 EP1033405-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 25-FEB-2000; 2000EP-0301439.  
 XX  
 PR 25-FEB-1999; 99US-0121825.  
 PR 05-MAR-1999; 99US-0123180.  
 PR 09-MAR-1999; 99US-0123548.  
 PR 23-MAR-1999; 99US-0125788.  
 PR 25-MAR-1999; 99US-0126264.  
 PR 29-MAR-1999; 99US-0126785.  
 PR 01-APR-1999; 99US-0127462.  
 PR 06-APR-1999; 99US-0128234.  
 PR

PR 08-APR-1999; 99US-0128714.  
 PR 16-APR-1999; 99US-0129845.  
 PR 19-APR-1999; 99US-0130077.  
 PR 21-APR-1999; 99US-0130449.  
 PR 23-APR-1999; 99US-0130510.  
 PR 28-APR-1999; 99US-0130891.  
 PR 30-APR-1999; 99US-0131449.  
 PR 30-APR-1999; 99US-0132048.  
 PR 30-APR-1999; 99US-0132407.  
 PR 04-MAY-1999; 99US-0132484.  
 PR 05-MAY-1999; 99US-0132485.  
 PR 06-MAY-1999; 99US-0132486.  
 PR 06-MAY-1999; 99US-0132487.  
 PR 07-MAY-1999; 99US-0132863.  
 PR 11-MAY-1999; 99US-0134256.  
 PR 14-MAY-1999; 99US-0134218.  
 PR 14-MAY-1999; 99US-0134219.  
 PR 14-MAY-1999; 99US-0134221.  
 PR 14-MAY-1999; 99US-0134370.  
 PR 18-MAY-1999; 99US-0134768.  
 PR 19-MAY-1999; 99US-0134941.  
 PR 20-MAY-1999; 99US-0135124.  
 PR 21-MAY-1999; 99US-0135353.  
 PR 24-MAY-1999; 99US-0135629.  
 PR 25-MAY-1999; 99US-0136021.  
 PR 27-MAY-1999; 99US-0136392.  
 PR 28-MAY-1999; 99US-0136782.  
 PR 01-JUN-1999; 99US-0137222.  
 PR 03-JUN-1999; 99US-0137528.  
 PR 04-JUN-1999; 99US-0137502.  
 PR 07-JUN-1999; 99US-0137724.  
 PR 08-JUN-1999; 99US-0138094.  
 PR 10-JUN-1999; 99US-0138540.  
 PR 10-JUN-1999; 99US-0138847.  
 PR 14-JUN-1999; 99US-0139119.  
 PR 16-JUN-1999; 99US-0139452.  
 PR 16-JUN-1999; 99US-0139453.  
 PR 17-JUN-1999; 99US-0139492.  
 PR 18-JUN-1999; 99US-0139454.  
 PR 18-JUN-1999; 99US-0139455.  
 PR 18-JUN-1999; 99US-0139456.  
 PR 18-JUN-1999; 99US-0139457.  
 PR 18-JUN-1999; 99US-0139458.  
 PR 18-JUN-1999; 99US-0139459.  
 PR 18-JUN-1999; 99US-0139460.  
 PR 18-JUN-1999; 99US-0139461.  
 PR 18-JUN-1999; 99US-0139462.  
 PR 18-JUN-1999; 99US-0139463.  
 PR 18-JUN-1999; 99US-0139750.  
 PR 18-JUN-1999; 99US-0139763.  
 PR 21-JUN-1999; 99US-0139817.  
 PR 22-JUN-1999; 99US-0139899.  
 PR 23-JUN-1999; 99US-0140353.  
 PR 23-JUN-1999; 99US-0140354.  
 PR 24-JUN-1999; 99US-0140695.  
 PR 24-JUN-1999; 99US-0140823.  
 PR 29-JUN-1999; 99US-0140991.  
 PR 30-JUN-1999; 99US-0141287.  
 PR 01-JUL-1999; 99US-0141842.  
 PR 01-JUL-1999; 99US-0142154.  
 PR 02-JUL-1999; 99US-0142055.  
 PR 06-JUL-1999; 99US-0142390.  
 PR 08-JUL-1999; 99US-0142803.  
 PR 09-JUL-1999; 99US-0142920.  
 PR 12-JUL-1999; 99US-0142977.  
 PR 13-JUL-1999; 99US-0143542.  
 PR 14-JUL-1999; 99US-0143624.  
 PR 15-JUL-1999; 99US-0144005.  
 PR 16-JUL-1999; 99US-0144085.  
 PR 16-JUL-1999; 99US-0144086.  
 PR 19-JUL-1999; 99US-0144325.  
 PR 19-JUL-1999; 99US-0144331.  
 PR 19-JUL-1999; 99US-0144332.



Db 1125 AAGCTACTACAGTCACAAACCATCGGTTGTCTGTCAGTGAGGAAACATGTGGAGAGCATC 1184  
 Qy 1349 ACATGACCTAAGGCTGTGATCACAACCTTATGAGGAAAGCACAACCATGATGTTCTCTGC 1408  
 Db 1185 ACACGACATGAGAGCAGTAAATCAACCTACGAAAGGAAACACAACCATGATGTTCTCTGC 1244  
 Qy 1409 AGCCCGTGGCAGTGG 1423  
 Db 1245 AGCTCGTGTAGCGG 1259

## RESULT 7

ABZ12999

ID ABZ12999 standard; DNA; 1539 BP.

XX

AC

XX

XX

21-JAN-2003 (first entry)

XX

DE Arabidopsis thaliana stress regulated gene SEQ ID NO 804.

XX

KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX

OS Arabidopsis thaliana.

XX

PN WO200216655-A2.

XX

PD 28-FEB-2002.

XX

PP 24-AUG-2001; 2001WO-US26685.

XX

PR 24-AUG-2000; 2000US-227866P.

XX

PR 28-JAN-2001; 2001US-284647P.

XX

PR 22-JUN-2001; 2001US-300111P.

XX

PA (SCRI ) SCRIPPS RES INST.

XX

PA (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX

PI Harper JF, Kreps J, Wang X, Zhu T;

XX

PS WPI; 2002-304127/34.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Qy 770 AAGAAGTTATTACAAATGCACATACCCCAATTCCTTACAAAGAAAGAGTTGAGAGTTC 829  
 Db 588 TCGGAGTTACTATAAGTGTACTTTCCCTAAATGTCCACGAAGAAGAAGTGGAGAGATC 647  
 Qy 830 TTTAGATGGACAAATTAAGTGTACTTATAGGAGTACTATACCACTCCTTAAGCCTCA 889  
 Db 648 TTTGGAAGGTCAAGTACAGAGATTTGTATTAAGGAAGCCCAACCATCTCTAAACCTCA 707  
 Qy 890 AAATCTAGGAGAAACTCATCAAACTCCCTCTTCTCTTGCATATCCCTCATTTCAAAATTCAT 949  
 Db 708 GTCTACTAGAGATCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 767  
 Qy 950 CAGAACTGAAATCC-----CAGATCAATCTTATGCCACACATGGAGTGGACA 997  
 Db 768 TTTGGATCATATCGTCAAGCTTCTCTGATCAGCTTAATTCCTCAATATAGCTTTTCATCA 827  
 Qy 998 AATGATTCAGCTGCCACCCAGAA-----AACTCATCAATATCAATTTGGAGATCA 1048  
 Db 828 GTCTGATTCCTTTGGGATGCAACNAGAGGATTAATCTACTTCTGATTTCTGTTGGTGACCA 887  
 Qy 1049 TGATTTTGAGCAGAGTTCCCAAAAGTGTAAATCAGGAGGGGATGAATATGATGAAGATCA 1108  
 Db 888 TGAGTTCGAACCAAGGCTC---ATCGATTTGTACGAGAGACGAGAGAGATTTGGGAGTCA 944  
 Qy 1109 ACCTGATGCCAAAAGATGGAAAATTTGAAGGTGAAAATAGGGGTATGTTCAGCCCTTGGAAAG 1168  
 Db 945 ACCTGAAGCAAGAGATGGAAAGGGGACAATGAAACAAATGGTGGGAATGGTGGTGGAAAG 1004  
 Qy 1169 TAGAACAGTGGAGAGAACCTTAGAGTTGTAGTTTTCAGACCAACAGTACATTTGATCTCTCA 1228  
 Db 1005 CAAGACAGTGGAGAGCCGAGAAATCGTAGTCAGACCAACGNGTGTATTTGACATTTCTTGA 1064  
 Qy 1229 TGATGGCTATAGTGGAGAAAATACGGGCAGAAAAGTAGTGAAGGGCAATCCCAATCCAAG 1288  
 Db 1065 CGACGGTTACAGATGGAGAAAATACGGCCAGAAAAGTCTTTAGGGGAAAACCCAAATCCAAG 1124  
 Qy 1289 GAGTTTACTACAAAGTGCACACACCCAGGATGTCCAGTGGAGAAAGCAGTGGAAAGAGCCTC 1348  
 Db 1125 AAGCTACTACAAAGTGCACAAACCATCGGTTGTCCAGTGGAGGAAACATGTGGAGAGCATC 1184  
 Qy 1349 ACATGACCTAAGGCTGTGATCACAACCTTATGAGGAAAGCACAACCATGATGTTCTCTGC 1408  
 Db 1185 ACACGACATGAGAGCAGTAAATCAACCTACGAAAGGAAACACAACCATGATGTTCTCTGC 1244  
 Qy 1409 AGCCCGTGGCAGTGG 1423  
 Db 1245 AGCTCGTGTAGCGG 1259

## RESULT 8

ABZ13876

ID ABZ13876 standard; DNA; 1182 BP.

XX

AC

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Claim 144; SEQ ID NO 804; 577pp + Sequence Listing; English.

The invention relates to identifying a stress condition to which a plant

cell has been exposed, comprising:

(a) contacting nucleic acid representative of expressed polynucleotides

in the plant cell with an array or probes representative of the plant

cell genome; and

(b) detecting a profile of expressed polynucleotides in the plant cell

characteristic of a stress response. The method is useful in the

production of transgenic plants, cells and seeds and in producing plants

with increased tolerance to abiotic stress. The present sequence is that

of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used

in methods of the invention.

Note: The sequence data for this patent is not represented in the printed

specification but is based on sequence information supplied to Derwent by

the European Patent Office.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Query Match 16.0%; Score 308.2; DB 24; Length 1539;

Best Local Similarity 67.1%; Pred. No. 2.9e-70;

Matches 493; Conservative 0; Mismatches 218; Indels 24; Gaps 3;

710 AGATGATGGGTACAAATTTGGAGGAAATATGGCCAAAACCAAGTGAAGGAGTGAATCC 769

528 AGAGGATGGTTACAAATTTGGAGGAAATATGGCCAAAACCAAGTGAAGGAGTGAATCC 587



PA (SCRI ) SCRIPPS RES INST.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX Harper JF, Kreps J, Wang X, Zhu T;  
XX WPI; 2002-304127/34.  
XX  
XX Identifying a stress condition to which a plant cell has been exposed  
XX and producing plants with increased tolerance to these abiotic stresses  
XX  
XX Claim 144; SEQ ID NO 1681; 577pp + Sequence Listing; English.  
XX  
XX The invention relates to identifying a stress condition to which a plant  
XX cell has been exposed, comprising:  
XX (a) contacting nucleic acid representative of expressed polynucleotides  
XX in the plant cell with an array or probes representative of the plant  
XX cell genome; and  
XX (b) detecting a profile of expressed polynucleotides in the plant cell  
XX characteristic of a stress response. The method is useful in the  
XX production of transgenic plants, cells and seeds and in producing plants  
XX with increased tolerance to abiotic stress. The present sequence is that  
XX of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used  
XX in methods of the invention.  
XX Note: The sequence data for this patent is not represented in the printed  
XX specification but is based on sequence information supplied to Derwent by  
XX the European Patent Office.  
XX  
XX Sequence 1182 BP; 374 A; 231 C; 265 G; 312 T; 0 other;  
XX  
XX Query Match 14.0%; Score 270.2; DB 24; Length 1182;  
XX Best Local Similarity 63.3%; Pred. No. 2.3e-60;  
XX Matches 463; Conservative 0; Mismatches 238; Indels 30; Gaps 2;  
XX  
QY 683 ACAATCTCAGACTTAAAGTAGAGGTGACATGATGGTACATTCGAGCAATATCGCCA 742  
Db 468 ACCAGATACATGGTGAAGAGGAACTTAATGATGTTGTTGAGAAATACGGTCA 527  
QY 743 AAAACAAGTGAAGGGAAGTCAAAATCCAGAACTTATTACAAATGCACATACCCCAATTG 802  
Db 528 GAAACAAGTGAAGAGGCAAAACCTAGGATTTACTTCAAGTGTACGTATCCTGATTG 587  
QY 803 CCTACAAAGAAGAGGTTGAGAGGCTTTTAGATGGACAAATTTACTGAGATGTTTATAA 862  
Db 588 TGTTTCCAAGAGATTGTTGAGACGGCTTCTGATGACAGATCACTGAGATCATTTATAA 647  
QY 863 GGGTACTCTAACCATCTTAAGCTCAAAATAGTACAGGAACTCATCAACTCTCTTC 922  
Db 648 AGGTGTCATATCATCTTAAGCTGAGTTCACCAAGAGA----- 687  
QY 923 TCTTGCATCCCTCAATTCATTCATCAGAACTGAAATCCAGATCAATCTATGCCAC 982  
Db 688 -----CCATCTCATCTTATACATCATCGTTAATGGAGGCGCTTGTATTC-- 740  
QY 983 ACATGAAGTGGCAAAATGATTCAGCTGCCACCCAGAAAATCTATCAATATCAATTGG 1042  
Db 741 ---TGCTTCTGTTAGTGAACCTCATGATCAATCAGAGAACTCTTCGATTTCGTTGA 797  
QY 1043 AGATGATGATTTTGACAGAGATTCACCAAGTGAATTAATCAGAGGGGATGAATGATGA 1102  
Db 798 CTATAGTATCTTTGACAGCAAAAGTTTAAATCAGAGTATGTTGATAGATGAAGAGGA 857  
QY 1103 AGATGAACCTGATGCCAAAGATGGAATTTGAAGGTGAAATGAGGGTATGTGACGCC 1162  
Db 858 GGAAACCTGATGATGAAGAGGATGAAGAGAGGTTGAAGATGAAGGGATGCTATAGA 917  
QY 1163 TGAAGTAGAAGTGAAGAGAACTTGAAGTTGATGTTTCAGACCAACCACTGACATTCAT 1222  
Db 918 AGTAACAAAGGAGTTAAAGAGCCAAAGTTGTTGTTTCAGACAAATAGTATGATGCT 977  
QY 1223 CCTTGATGATGCTATGATGGAAGAAATACGGGCGAAGAGTAGTGAAGGCAATCAAA 1282  
Db 978 TCTTATAGATGGCTTTAGATGGAGGAATATGCTCAAAAGTTTGTCAAAGGAATACTAA 1037

QY 1283 TCCAAAGGAGTACTACAGTGCACACACCCAGGATGTCAGTGAGCAACGTCGAAAG 1342  
Db 1038 TCCAAAGGAGTACTACAGTGCACATTCCTCAAGGTTGTGAGTGAAGCAAGTGAAG 1097  
QY 1343 AGCTTCACATGACCTTAAGGGCTGTGATCACTTATGAGGGAAGCAACCATGATGT 1402  
Db 1098 ATCCCGCAGCAGAGAGAGAGCAGTTCCTCACTACCTATGAGGAAGACACAATCAGATAT 1157  
QY 1403 TCCTGCAGCCC 1413  
Db 1158 CCAACCCGGC 1168  
XX  
XX RESULT 9  
XX AAC40213  
XX ID AAC40213 standard; DNA; 1589 BP.  
XX AC AAC40213;  
XX DT 17-OCT-2000 (first entry)  
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 27480.  
XX KW Hybridisation assay; genetic mapping; gene expression control;  
XX protein identification; signal transduction pathway;  
XX metabolic pathway; promoter; termination sequence; ss.  
XX OS Arabidopsis thaliana.  
XX PN EP1033405-A2.  
XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-0301439.  
XX PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.  
PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
PR 23-APR-1999; 99US-0130510.  
PR 28-APR-1999; 99US-0130891.  
PR 30-APR-1999; 99US-0131449.  
PR 30-APR-1999; 99US-0132048.  
PR 04-MAY-1999; 99US-0132407.  
PR 05-MAY-1999; 99US-0132484.  
PR 06-MAY-1999; 99US-0132485.  
PR 06-MAY-1999; 99US-0132486.  
PR 06-MAY-1999; 99US-0132487.  
PR 07-MAY-1999; 99US-0132863.  
PR 11-MAY-1999; 99US-0134256.  
PR 14-MAY-1999; 99US-0134218.  
PR 14-MAY-1999; 99US-0134219.  
PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
PR 18-MAY-1999; 99US-0134768.  
PR 19-MAY-1999; 99US-0134941.  
PR 20-MAY-1999; 99US-0135124.  
PR 21-MAY-1999; 99US-0135353.  
PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.  
 PR 07-JUN-1999; 99US-0137724.  
 PR 08-JUN-1999; 99US-0138094.  
 PR 10-JUN-1999; 99US-0138540.  
 PR 10-JUN-1999; 99US-0138847.  
 PR 14-JUN-1999; 99US-0139119.  
 PR 16-JUN-1999; 99US-0139452.  
 PR 16-JUN-1999; 99US-0139453.  
 PR 17-JUN-1999; 99US-0139492.  
 PR 18-JUN-1999; 99US-0139454.  
 PR 18-JUN-1999; 99US-0139455.  
 PR 18-JUN-1999; 99US-0139456.  
 PR 18-JUN-1999; 99US-0139457.  
 PR 18-JUN-1999; 99US-0139458.  
 PR 18-JUN-1999; 99US-0139459.  
 PR 18-JUN-1999; 99US-0139460.  
 PR 18-JUN-1999; 99US-0139461.  
 PR 18-JUN-1999; 99US-0139462.  
 PR 18-JUN-1999; 99US-0139463.  
 PR 18-JUN-1999; 99US-0139750.  
 PR 18-JUN-1999; 99US-0139763.  
 PR 21-JUN-1999; 99US-0139817.  
 PR 22-JUN-1999; 99US-0139899.  
 PR 23-JUN-1999; 99US-0140353.  
 PR 23-JUN-1999; 99US-0140354.  
 PR 24-JUN-1999; 99US-0140595.  
 PR 28-JUN-1999; 99US-0140823.  
 PR 29-JUN-1999; 99US-0140991.  
 PR 30-JUN-1999; 99US-0141287.  
 PR 01-JUL-1999; 99US-0141842.  
 PR 01-JUL-1999; 99US-0142154.  
 PR 02-JUL-1999; 99US-0142055.  
 PR 06-JUL-1999; 99US-0142390.  
 PR 08-JUL-1999; 99US-0142803.  
 PR 09-JUL-1999; 99US-0142920.  
 PR 12-JUL-1999; 99US-0142977.  
 PR 13-JUL-1999; 99US-0143542.  
 PR 14-JUL-1999; 99US-0143624.  
 PR 15-JUL-1999; 99US-0144005.  
 PR 16-JUL-1999; 99US-0144085.  
 PR 16-JUL-1999; 99US-0144086.  
 PR 19-JUL-1999; 99US-0144325.  
 PR 19-JUL-1999; 99US-0144331.  
 PR 19-JUL-1999; 99US-0144332.  
 PR 19-JUL-1999; 99US-0144333.  
 PR 19-JUL-1999; 99US-0144334.  
 PR 19-JUL-1999; 99US-0144335.  
 PR 20-JUL-1999; 99US-0144352.  
 PR 20-JUL-1999; 99US-0144632.  
 PR 20-JUL-1999; 99US-0144884.  
 PR 21-JUL-1999; 99US-0144814.  
 PR 21-JUL-1999; 99US-0145086.  
 PR 21-JUL-1999; 99US-0145088.  
 PR 22-JUL-1999; 99US-0145085.  
 PR 22-JUL-1999; 99US-0145087.  
 PR 22-JUL-1999; 99US-0145089.  
 PR 22-JUL-1999; 99US-0145132.  
 PR 23-JUL-1999; 99US-0145145.  
 PR 23-JUL-1999; 99US-0145218.  
 PR 23-JUL-1999; 99US-0145224.  
 PR 26-JUL-1999; 99US-0145276.  
 PR 27-JUL-1999; 99US-0145913.  
 PR 27-JUL-1999; 99US-0145918.  
 PR 27-JUL-1999; 99US-0145919.  
 PR 28-JUL-1999; 99US-0145951.  
 PR 02-AUG-1999; 99US-0146386.  
 PR 02-AUG-1999; 99US-0146388.  
 PR 02-AUG-1999; 99US-0146389.  
 PR 03-AUG-1999; 99US-0147038.  
 PR 04-AUG-1999; 99US-0147204.  
 PR 04-AUG-1999; 99US-0147302.  
 PR 05-AUG-1999; 99US-0147192.  
 PR 05-AUG-1999; 99US-0147260.

PR 06-AUG-1999; 99US-0147303.  
 PR 06-AUG-1999; 99US-0147416.  
 PR 09-AUG-1999; 99US-0147493.  
 PR 09-AUG-1999; 99US-0147935.  
 PR 10-AUG-1999; 99US-0148171.  
 PR 11-AUG-1999; 99US-0148319.  
 PR 12-AUG-1999; 99US-0148341.  
 PR 13-AUG-1999; 99US-0148565.  
 PR 13-AUG-1999; 99US-0148684.  
 PR 16-AUG-1999; 99US-0149368.  
 PR 17-AUG-1999; 99US-0149175.  
 PR 18-AUG-1999; 99US-0149426.  
 PR 20-AUG-1999; 99US-0149722.  
 PR 20-AUG-1999; 99US-0149723.  
 PR 20-AUG-1999; 99US-0149929.  
 PR 23-AUG-1999; 99US-0149902.  
 PR 23-AUG-1999; 99US-0149930.  
 PR 25-AUG-1999; 99US-0150566.  
 PR 26-AUG-1999; 99US-0150884.  
 PR 27-AUG-1999; 99US-0151065.  
 PR 27-AUG-1999; 99US-0151066.  
 PR 27-AUG-1999; 99US-0151080.  
 PR 30-AUG-1999; 99US-0151303.  
 PR 31-AUG-1999; 99US-0151438.  
 PR 01-SEP-1999; 99US-0151930.  
 PR 07-SEP-1999; 99US-0152363.  
 PR 10-SEP-1999; 99US-0153070.  
 PR 13-SEP-1999; 99US-0153758.  
 PR 15-SEP-1999; 99US-0154018.  
 PR 16-SEP-1999; 99US-0154039.  
 PR 20-SEP-1999; 99US-0154779.  
 PR 22-SEP-1999; 99US-0155139.  
 PR 23-SEP-1999; 99US-0155486.  
 PR 24-SEP-1999; 99US-0155659.  
 PR 28-SEP-1999; 99US-0156458.  
 PR 29-SEP-1999; 99US-0156596.  
 PR 04-OCT-1999; 99US-0157117.  
 PR 05-OCT-1999; 99US-0157753.  
 PR 06-OCT-1999; 99US-0157865.  
 PR 07-OCT-1999; 99US-0158029.  
 PR 08-OCT-1999; 99US-0158232.  
 PR 12-OCT-1999; 99US-0158369.  
 PR 13-OCT-1999; 99US-0159293.  
 PR 13-OCT-1999; 99US-0159294.  
 PR 13-OCT-1999; 99US-0159295.  
 PR 14-OCT-1999; 99US-0159329.  
 PR 14-OCT-1999; 99US-0159330.  
 PR 14-OCT-1999; 99US-0159331.  
 PR 14-OCT-1999; 99US-0159637.  
 PR 14-OCT-1999; 99US-0159638.  
 PR 18-OCT-1999; 99US-0159584.  
 PR 21-OCT-1999; 99US-0160741.  
 PR 21-OCT-1999; 99US-0160767.  
 PR 21-OCT-1999; 99US-0160768.  
 PR 21-OCT-1999; 99US-0160770.  
 PR 21-OCT-1999; 99US-0160814.  
 PR 21-OCT-1999; 99US-0160815.  
 PR 22-OCT-1999; 99US-0160980.  
 PR 22-OCT-1999; 99US-0160981.  
 PR 22-OCT-1999; 99US-0160989.  
 PR 25-OCT-1999; 99US-0161404.  
 PR 25-OCT-1999; 99US-0161405.  
 PR 25-OCT-1999; 99US-0161406.  
 PR 26-OCT-1999; 99US-0161359.  
 PR 26-OCT-1999; 99US-0161360.  
 PR 26-OCT-1999; 99US-0161361.  
 PR 28-OCT-1999; 99US-0161920.  
 PR 28-OCT-1999; 99US-0161992.  
 PR 28-OCT-1999; 99US-0161993.  
 PR 29-OCT-1999; 99US-0162142.

Query Match 13.4%; Score 259.2; DB 21; Length 1589;  
 Best Local Similarity 62.3%; Pred. No. 2.1e-57;

Matches 472; Conservative 1; Mismatches 254; Indels 31; Gaps 3;	
QY 683	ACAATCTCAGACTTTTAAGTAGAAGGTGAGATGATGGGTACAAATGAGGAAATATGCGCA 742
Db 559	ACCAGCATACATGATGAGTAGGAACCTTAATGATGGTTATGGTGGAGAAATACGGTCA 618
QY 743	AAACAAGTGAAGGGAAGTGAATAATCAAGAAGTTATTACAAATGACACATACCCCAATTG 802
Db 619	GAACAAGTGAAGAAGGCGAAGAACCTTAGAGGTTACTTCAAGTGATCGGTATCTCTGATTG 678
QY 803	CCCTACAAAGAAGAGTGTGAGAGGCTTTAGATGGACAAATTTACTGAGATAGTTTATAA 862
Db 679	TGTTTCAAGAGAGTTGTGAGACGGCTTCTGATGACAGATCACATGAGATCAATTATAA 738
QY 863	GGGTACTCATAAACCATCTTAAGCCTCAAAATATCTAGGAGAAACTCATCAAACTCTCTTTC 922
Db 739	AGGTGTCATAATCATCTTAAGCCTGAGTTCACCAAGAGA----- 778
QY 923	TCATTGAATCCCTCATTCATAATTCATGACAACTGAAATCCCGAGATCAATCTTATGCCAC 982
Db 779	-----CCATCTCAATCTTCATTACCATCATCGGTTAATGGAGCGCTTGTGTTAATCC-- 831
QY 983	ACATGGAAGTGGACAATGATTCAGTCCGCCCCAGAAAACCTCATCAATCAATTCG 1042
Db 832	---TGCTTCTGTTGTAGTGAACCTCATGATCAATCAGAGAACTCTTCGATTTGCTTTGA 888
QY 1043	AGATGATGATTTTGGACAGAGTTTCCCAAAAGTGTAAATCAGAGGGGATGAATATATGCA 1102
Db 889	CTATAGTATCTTTGACGACAGAAAGTTTAAATCAGAGTATGGTGAGATAGTGAAGAGA 948
QY 1103	AGATGAACCTGATGCCAAAGATGGAATAATTGAAGTGAATAATGAGGGTATGTCAGCCCC 1162
Db 949	GGAAACAACCTGATCAAGAGAGTGAAGAGAGAGTGAAGATGAAGGGATGCTATAGA 1008
QY 1163	TGGAAGTAGACAGTG-AGAGAACCTAGAGTTCTAGTTCAGACAAACAGTGCATTCATA 1221
Db 1009	AGTAAGCAAGGAGTTTAAAGAGCCAGAGTGTGTTGTCAGACAAATAGTATGATGATG 1068
QY 1222	TCCTTGATGATGCTATAGTGTGAGAAATATACGGCAGAGAAAGTAGTGAAGGGCAATCCAA 1281
Db 1069	TTCATTATAGTGGCTTAGATGAGGAGAAATATGTTCAAAAGTTGTCAAGGNAATACTA 1128
QY 1282	ATCCAAGGAGTTACTACAAGTGCACACCCAGATGTCCAGTGAGGAGCAAGCTGGA 1341
Db 1129	ATCCAAGGAGTACTACAAGTGCACATTCCAAGTTGTGGAGTGAAGCAAGTGA 1188
QY 1342	GAGCTTCATGACCTTAAGGGCTGTGATCACACTTATAGGGAAGACCAACCATGATG 1401
Db 1189	GATCCCGCAGACGAGAGAGCAGTTCCTCACTACCTATGAAGGAAGACAAATCACGATA 1248
QY 1402	TTCTGTCAGCCCGTGGCAGTGGCAGCATTTCTGTGAAC 1439
Db 1249	TCCCAACCGCGCTACGTCGCTGTAATTTATGGGAC 1286

RESULT 10  
ABX26660  
ID ABX26660 standard; cDNA; 265 BP.  
XX  
AC ABX26660;  
XX  
DT 11-FEB-2003 (first entry)  
XX  
DE Human GDP-mannose 4,6-dehydratase (GM4,6D) DNA #8717.  
XX  
KW Human; GDP-mannose 4,6-dehydratase; GM4,6D; gene; ss; inflammation;  
KW cellular fucosylation; glycoconjugate fucosylation; transplant rejection;  
KW arthritis; asthma; sepsis; reperfusion injury; stroke; infection;  
KW complex carbohydrate; gene replacement therapy; immunosuppressive;  
KW antiinflammatory; antiarthritic; antibacterial; cerebroprotective;  
KW antiasthmatic; vasotropic.  
XX  
OS Homo sapiens.

XX PN US2002110548-A1.	
XX PD 15-AUG-2002.	
XX PF 11-JUN-2001; 2001US-0878574.	
XX PR 22-NOV-1996; 96US-0753233.	
PR 03-DEC-1997; 97US-0984246.	
PR 09-SEP-1998; 98US-0149674.	
PR 14-JUN-1999; 99US-0333177.	
XX (GEMY ) GENETICS INST INC.	
XX Sullivan F, Kriz R, Kumar R;	
XX WPI; 2003-066673/06.	
XX New composition comprising GDP-mannose 4,6-dehydratase (GM4,6D)	
PT peptide, for manufacturing complex carbohydrates, or as targets for	
PT screening GM4,6D antagonists for treating e.g. arthritis, or transplant	
PT rejection	
XX Disclosure; SEQ ID NO 8719; 6pp; English.	
XX The invention relates to a composition comprising a human GDP-mannose	
CC 4,6-dehydratase (GM4,6D) peptide. The peptide is useful for identifying	
CC GM4,6D inhibitors. GM4,6D inhibitors are useful for reducing inflammation	
CC in a mammalian subject and for treating or ameliorating diseases affected	
CC by the level of cellular fucosylation or diseases affected by the	
CC fucosylation of glycoconjugates. These diseases include arthritis,	
CC transplant rejection, asthma, sepsis, reperfusion injury, stroke or	
CC infection. The GM4,6D peptide or a polynucleotide encoding it is also	
CC useful for manufacturing complex carbohydrates and as targets for	
CC screening small molecule antagonists of the activity of the enzyme. The	
CC polynucleotide is useful in developing an assay for defects in the	
CC enzyme, as well as in gene replacement therapy. Sequences	
CC ABX17942-ABX17944 and ABX17947-ABX17916 represent DNA molecules encoding	
CC human GM4,6D peptides of the invention.	
CC Note: The sequence data for this patent did not form part of the printed	
CC specification but was obtained in electronic format directly from USPTO	
CC at seqdata.uspto.gov/sequence.html.	
XX Sequence 265 BP; 89 A; 56 C; 58 G; 62 T; 0 other;	
Query Match 13.3%; Score 256; DB 25; Length 265;	
Best Local Similarity 98.1%; Pred. No. 6.1e-57;	
Matches 259; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
QY 510 ACACACAGCCATGGAGTTTTCAGGAGCCAGAAACAGGATAATTTTCTCAGGAAAG 569	
Db 2 ACACACAGCCATGGAGTTTTCAGGAGCCAGAAACAGGATAATTTTCTCAGGAAAG 61	
QY 570 GGTATGATGAAACCTGAAACCTCTTCTTCATGAGAGTTTTCCTGAGATGCTAGT 629	
Db 62 GGTATGATGAAACCTGAAACCTCTTCTTCATGAGAGTTTTCCTGAGATGCTAGT 121	
QY 630 GTCCAAACTAACCATAGCAATGGGTTTCAATCCGATATGGCAATTACCCCAATCT 689	
Db 122 GTCCAAACTAACCATAGCAATGGGTTTCAATCCGATATGGCAATTACCCCAATCT 181	
QY 690 CAGACTTTTAAAGTAGAAGGTTCAGATGATGGTACAAATTGGAGGAAATATGCCAAAAACAA 749	
Db 182 CAGACTTTTAAAGTAGAAGGTTCAGATGATGGTACAAATTGGAGGAAATATGGTCAAAACCA 241	
QY 750 GTGAAGGGAAGTGAATAATCCAAAGA 773	
Db 242 GTGAAGGGAAGTGAATAATCCAAAGA 265	
RESULT 11	
ABX59412	
ID ABX59412 standard; cDNA; 2343 BP.	

XX AC ABS59412;  
XX DT 05-NOV-2002 (first entry)  
XX DE Soybean WRKY polynucleotide #2.  
XX DE WRKY; gene; ss; plant; zinc-finger-type factor; WRKY; SAR; sunflower;  
KW SA-dependent structure-activity analysis response; pathogen resistance;  
KW maize; wheat; rice; soybean.  
XX OS Glycine max.  
XX PN US2002076775-A1.  
XX PD 20-JUN-2002.  
XX PF 16-MAR-2001; 2001US-0810264.  
XX PR 17-MAR-2000; 2000US-190467P.  
XX PA (CRAN/) CRANE V C.  
XX PA (FAMO/) FAMODU O.  
XX PA (HUX/) HU X.  
XX PA (LUGG/) LU G.  
XX PA (ZHAN/) ZHANG L.  
XX PI Crane VC, Famodu O, Hu X, Lu G, Zhang L;  
XX DR WPI; 2002-582922/62.  
XX DR P-PSDB; ABG76916.  
XX PT New isolated plant-specific zinc-finger-type factor polynucleotide,  
XX PT useful for e.g. regulating the SA-dependent structure-activity analysis  
XX PT response in a plant  
XX PS Claim 21; Page 47-48; 66pp; English.  
XX CC The invention relates to an isolated polynucleotide encoding a  
CC plant-specific zinc-finger-type factor (WRKY) protein. The DNA and  
CC protein are used to modulate the level of a WRKY protein in a plant and  
CC to regulate the SA-dependent structure-activity analysis (SAR) response  
CC in a plant. The sequences can be used to engineer plants to resist  
CC pathogens such as viruses, bacteria, insects and fungi, and to survive  
CC stress. They may also be used as a molecular probe to track inheritance  
CC of corresponding loci in genetic crosses and facilitate the plant  
CC breeding process, to isolate, identify and genetically map WRKY and other  
CC closely related disease resistance genes and to find genes and their  
CC promoters that respond to a WRKY domain. This sequence represents DNA  
CC encoding a WRKY polypeptide of the invention.  
XX SQ Sequence 2343 BP; 717 A; 527 C; 482 G; 617 T; 0 other;  
Query Match 12.1%; Score 232.8; DB 24; Length 2343;  
Best Local Similarity 59.5%; Pred. No. 2e-50;  
Matches 437; Conservative 0; Mismatches 282; Indels 15; Gaps 2;  
QY 703 GAAGGTGAGTGGGTACAAATGGAGGAAATATGGCCAAACAAAGTGAAGGAGTG 762  
DB 867 GAGTATCTGATGGATACAACTGGAGAAATATGGCCAAACAAATGTTAAAGGAAGTG 926  
QY 763 AAAATCAAGAGTTATTACAAATGCAATCCCAATTTGGCCCTACAAAGAGAGTTG 822  
DB 927 AATTTCCACGCGATTATTACAAATGTACATCTCTAATGTGAAGTTAAGAAACTATTTG 986  
QY 823 AGAGGTCTTTAGTGGCAATTTACTGAGATGTTTATAGGGTACTCATACCATCCTA 882  
DB 987 AACGCTCCCATGATGGCAAAATCACTGAGATAATTTACAGGGAACACATGATCATCTTA 1046  
QY 883 AGCCTCAAAATPACTAGGAGAACTCATCAAACTCCTCTCTCTTTCGAAATCCCTCATTTCAA 942  
DB 1047 AACCTCAACGAACCGCGTTACTCTGAGGAATATAATGCTGTGCAAGAGACAGAT 1106

QY 943 ATTCATCAGAACTGAAATCCAGATCAATCCTATGCCACATGGAAGTGCACAAATG- 1001  
DB 1107 CTGATAAGCTTCTTTGACTAGCCGAGATGACAAAGGATCCAAATATGTGTGCGCAGGGGT 1166  
QY 1002 -----GATTCAGCTGCCACCCAGAAAACATCATCAATATCAATTTGGAGATG 1050  
DB 1167 CTCACCTGGCTGAGCCCGGTAACACAGAGTTTATGCTGTAGCAACAAATGATGGTG 1226  
QY 1051 ATTTTGACGAGATTTCCCAAAAGTCTAAATCAGGAGGGGATGAATATGATGAAGATGAAC 1110  
DB 1227 ATCTAGATGTTTGGGGGTTTTGTCAACCGGAATATGATGAGGTTGATGATGATGATC 1286  
QY 1111 CTGATGCCAAAAGATGGAATTTGAAGGTGAAATGAGGGTATGTCAGCCCCCTGGAAATG 1170  
DB 1287 CTTTCTCAAGCGAAGAAAATGGACGTTGGAATTTGCTGACAT---CACTCTCTGATGTTA 1343  
QY 1171 GAACAGTGAAGAACCTGAGTTGATGTTTTCAGACAAACCGTGCACATTTGATATCTCTTGTG 1230  
DB 1344 AGCCTATCCGGGAGCCACGTTGTTGTACAAACTCTGAGTGAGGTTGATATCTCTTGGATG 1403  
QY 1231 ATGGCTATAGTGGAGAAATACGGGCGAGAAATAGTAGGAGGCAATCCAAATCCAAGGA 1290  
DB 1404 ATGGCTATCGCTGGCGCAAGTATGGCGAAGGTTGGTAGAGGCAATCCTAACCTTAGGA 1463  
QY 1291 GTTACTACAAAGTGCACACACCCAGGATGTCAGTGAGGAGGACGCTGGAAAGAGCCTCAC 1350  
DB 1464 GTTATTACAAATGCACGACACCGGTTGCCCGTTAGAAAAACACGTTGAGAGGGCATCTC 1523  
QY 1351 ATGACCTAAGGGCTGTGATCACAATTTATGAGGAAAGACAAACCATGATTTCTTGCAG 1410  
DB 1524 ATGATCCAAAGCTGTGATTACGATGATGAGGGGAAACACAAATCATGATGTACCAACTG 1583  
QY 1411 CCCGTGGCAGTGGC 1424  
DB 1584 CAAGGAATAGTTGC 1597

RESULT 12

ABZ12620  
ID ABZ12620 standard; DNA; 1542 BP.  
XX AC ABZ12620;  
XX DT 21-JAN-2003 (first entry)  
XX DE Arabidopsis thaliana stress regulated gene SEQ ID NO 425.  
XX KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.  
XX OS Arabidopsis thaliana.  
XX PN WO200216655-A2.  
XX PD 28-FEB-2002.  
XX PF 24-AUG-2001; 2001WO-US26685.  
XX PR 24-AUG-2000; 2000US-227866P.  
XX PR 26-JAN-2001; 2001US-264647P.  
XX PR 22-JUN-2001; 2001US-300111P.  
XX PA (SCRI ) SCRIPPS RES INST.  
XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX PI Harper JF, Kreps J, Wang X, Zhu T;  
XX WPI; 2002-304127/34.  
XX DR Identifying a stress condition to which a plant cell has been exposed  
XX PT and producing plants with increased tolerance to these abiotic stresses  
XX PT  
XX PS Claim 144; SEQ ID NO 425; 577pp + Sequence Listing; English.

XX  
CC The invention relates to identifying a stress condition to which a plant  
CC cell has been exposed, comprising:  
CC (a) contacting nucleic acid representative of expressed polynucleotides  
CC in the plant cell with an array or probes representative of the plant  
CC cell genome; and  
CC (b) detecting a profile of expressed polynucleotides in the plant cell  
CC characteristic of a stress response. The method is useful in the  
CC production of transgenic plants, cells and seeds and in producing plants  
CC with increased tolerance to abiotic stress. The present sequence is that  
CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used  
CC in methods of the invention.  
CC Note: The sequence data for this patent is not represented in the printed  
CC specification but is based on sequence information supplied to Derwent by  
CC the European Patent Office.

Sequence 1542 BP; 478 A; 332 C; 365 G; 367 T; 0 other;

Query Match 11.9%; Score 228.8; DB 24; Length 1542;  
Best Local Similarity 58.9%; Pred. No. 1.9e-49;  
Matches 442; Conservative 0; Mismatches 287; Indels 21; Gaps 2;

Qy	582	CACAACTCTCAGACTTTAAGTGTAGAGGTCAGATGATGGTCAAAATGTGAGAGGAATATGCGC	741
Db	719	CACAGCCTCAAAAATGCTGCACAAACCGCTGATGATGATACAACCTGCGGAAATATGGCG	778
Qy	742	AAAAACAAGTGAAGGGAAGTGAAAATCCAAGAAGTTATTACAAATGCACATACCCCAATT	801
Db	779	AGAAAGCAAGTGAAGGGAGCGATTTTCTCGAGTTATTACAAATGTACCGATCCAGCTT	838
Qy	802	GCCTTACAAAGAAAGAGGTTTGAGAGGCTTTTAGATGGACAAATTAATCTGAGATAGTATTATA	861
Db	839	GTCCTGTCAAGAAAGAAAGTGAGAGGTCACCTCGATGCACAAAGTAACGGAATCATCTACA	898
Qy	862	AGGCTACTCATAAACCATCTTAAGCCTCAAAATCTAGAGAGAACTCATCAAACTCCTCTT	921
Db	899	AGGGTCAACACAATCATGAGCTTCTCCAAAGCGCGGTAAACAATAACGGGAGTTGTAAAA	958
Qy	922	CTCTTGCAATCCCTCATTTCAAATCCCATCAGAACTGAAATCCCAAGATCAATCCCTATGCCA	981
Db	959	GTTCTGATATTGCAAAATCAGTTTCAACACAGTAATAGCAGTCTCCAAACAGAGTAAGAGG	1018
Qy	982	CACATGGAAGTGGACAAATGGAATTCAGTGCACCCAGAGAAAATCTCATCAATATCAATTG	1041
Db	1019	ACCAGGAAACAAGCCA-----AGTTACAACAACAGAGCAGATGCTCTCAGCAAGTG	1069
Qy	1042	GAGATGATGATTTTGAGCAGAGTTCCCAAAGTGTAAATCAGAGGGGATGAATATGATG	1101
Db	1070	ATACGCGAGGAGTTGGG-----AATGCAGAGACATAGTGTGGGAGAAAGACATG	1117
Qy	1102	AAGATGAACCTGATGCCAAAGATGGAATAATTGAAGTGTGAAATGAGGGTATGTACAGCCC	1161
Db	1118	AGGATGAGCCTGATCCCAAGCGAAGAAATACAGAAGTTTCGGGTTTCAGAACCGAGTTGCTT	1177
Qy	1162	CTGGAAGTAGAACAGTGTAGAGAACTTAGAGTTGTAGTTTCAGACAAACAGATGCATTTGATA	1221
Db	1178	CATCGCATAGAACTGTGCAGAGGCTTAGGATTATTGTCCAAAACGACAGTGAAGTTGACC	1237
Qy	1222	TCCTTGATGATGGCTATAGTGTGAGAAAAATACGGGCGAGAAAGTAGTGAAGGGCAATCCAA	1281
Db	1238	TCCTTAGATGATGATATAGGTGGCGCAAGTATGGTCAGAAAAGTAGTCAAAAGGAAATCCTT	1297
Qy	1282	ATCCAAGGAGTTACTACAAGTGCACACACCAGGATGTCCAGTGAGAGAACACCTGTGAAA	1341
Db	1298	ATCCGAGGAGCTACTATAAGTGTGTACAACACAGATTCGGAGTGAAGAAAACATGTAGAGA	1357
Qy	1342	GAGCCTCACATGACCTTAAGGCGCTGTGATCAAACTTATGAGGGAAGAACCAACCATCATG	1401
Db	1358	GAGCAGAACTGACCCAAAAGCTGTTGTAAACAACATATGAGGTAAACATAACCATGATG	1417
Qy	1402	TTCTCGAGCCCGTGGCAGTGCGCAGCCATT	1431
Db	1418	TTCCAGCTGCTAGAAACCGACGAGCCATCAGT	1447

QY 862 AGGTACTCATACCATCTTACGCTCAAAATCTAGGAGAACTCATCAAACTCCTCT 921  
 DB |||||  
 DB 899 AGGTCAACACATCATGAGCTTCTCAAAAGCGCGTAACTAACCGGAGTTGTA 958  
 QY 922 CTCTGCAATCCCTCATCAAAATCTCAATCAGAACTCCAGATCAATCCATG 981  
 DB |||||  
 DB 959 GTTCGATATGCAATCAGTTTCAACAAGTATAGCAGTCTCAACAAGAGTAAG 1018  
 QY 982 CACATGAAGTGACAAATGATTCAGTGCACCCAGAGAACTCATCAATATCA 1041  
 DB |||||  
 DB 1019 ACCAGGAAACAAGCCCA-----AGTTACAAACAAGCAGCAGATGCTG 1069  
 QY 1042 GAGATGATGTTTGAAGCAGAGTTCCCAAAAGTGAATCAAGAGGATGA 1101  
 DB |||||  
 DB 1070 ATAGCAGGAGGTTGGG-----AATCAGAGACTAGTGTGGGAGAAAG 1117  
 QY 1102 AAGATGAACCTGATGCCAAAGATGGAATTTGAAGTGAATGAGGGTATG 1161  
 DB |||||  
 DB 1118 AGGATGAGCTGATCCNAGCGAAGAAATACAGAAGTTCCGGGTTTCAGA 1177  
 QY 1162 CTGGAAGTAGAACAGTGAGAGAACTTGAAGTGTGATGTTGACAAACAG 1221  
 DB |||||  
 DB 1178 CATCGCATAGAACTGTGACAGAGCTAGGATTTATGTCCAAACGAGAG 1237  
 QY 1222 TCCTTGATGCTATAGTGGAGAAATACGGGAGAAAGTAGTGAAGGCAAT 1281  
 DB |||||  
 DB 1238 TCTTAGATGATGATATAGTGGCGCAAGTATGTCAGAAAGTAGTCAAG 1297  
 QY 1282 ATCAAGAGGAGTACTACAGTGACACACACCCAGGATGTCAGTGAGGA 1341  
 DB |||||  
 DB 1298 ATCCGAGGAGTACTATAGTGTACACACACAGATTCGGGAGTAAAG 1357  
 QY 1342 GAGCCTCACATGACCTAAGGCTGTGATACACTTATGAGGAAAGCACA 1401  
 DB |||||  
 DB 1358 GAGCAGCAACTGACCCAAAAGCTGTTGAACAACATAGAAAGTAAACA 1417  
 QY 1402 TTCTCGAGCCCGTGGCAGTGCGAGCCATT 1431  
 DB |||||  
 DB 1418 TTCAGCTGTAGAACCCAGCAGCCATCAGT 1447

RESULT 14

AD09830 standard; cDNA; 2158 BP.  
 ID AAD09830  
 AC AAD09830;  
 DT 12-SEP-2001 (first entry)  
 XX Wheat SPFI-related transcription factor #6 cDNA.  
 XX Wheat; SPFI-related transcription factor; transgenic plant;  
 KW genetical mapping; physical mapping; plant breeding; ss.  
 XX  
 XX  
 OS Triticum aestivum.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 3..1862  
 FT /\*tag= a  
 FT /product= "SPFI-related transcription factor #6"  
 FT /note= "CDS does not include start codon"  
 FT /partial

WO200149840-A2.

12-JUL-2001.

22-DEC-2000; 2000WO-US35310.

04-JAN-2000; 2000US-0174325.

(DUPO ) DU PONT DE NEMOURS & CO E I.

XX Zhu Q, Famodu OO, Rafalski JA;  
 PI WPI; 2001-441876/47.  
 DR P-PSDB; AAB05093.  
 XX Novel isolated SPFI-1 related transcription factor polypeptides and  
 DR polynucleotides useful for producing transgenic plants -  
 PT  
 XX Claim 7; Page 55-56; 60pp; English.  
 XX The present sequence is wheat SPFI-related transcription factor #6 cDNA.  
 CC The SPFI-related transcription factor is useful for transforming a cell  
 CC by introducing SPFI-related transcription factor into a cell. It is also  
 CC useful for producing a transgenic plant by transforming a plant cell with  
 CC SPFI-related transcription factor and regenerating a plant from the  
 CC transformed plant cell. It is also useful to create transgenic plants in  
 CC which SPFI-related transcription factor DNA is present at higher or lower  
 CC levels than normal or in cell types or developmental stages in which they  
 CC are not normally found. The SPFI-related transcription factor DNA is  
 CC useful to prepare antibodies. It is also used as probes for genetically  
 CC and physically mapping the genes that they are a part of, and used as  
 CC markers for traits linked to these genes. Such information is useful in  
 CC plant breeding in order to develop lines with desired phenotype.  
 XX  
 SQ Sequence 2158 BP; 596 A; 523 C; 549 G; 490 T; 0 other;

Query Match 11.5%; Score 221.6; DB 22; Length 2158;  
 Best Local Similarity 60.1%; Pred. No. 1.7e-47;  
 Matches 428; Conservative 0; Mismatches 269; Indels 15; Gaps 3;  
 QY 709 CAGATGATGGTACCAATTGGAGAAATATGGCAAAACAAAGTGAAGGGAAGTGA 768  
 DB |||||  
 DB 706 CAGATGATGGTACCAATTGGAGAAATATGGCAAAACAAAGTGAAGGGAAGTGA 765  
 QY 769 CAAGAAGTTATTACAAATCCACATACCCCAATTCGCCCTACAAAGAGAGAGTTG 828  
 DB |||||  
 DB 766 CTAGAAGTTATTACAAATCCACATACCCCAATTCGCCCTACAAAGAGAGAGTTG 825  
 QY 829 CTTTAGATGACAAATTAAGTGTATTAAGGTTACTCATACCATCCTTAAGCCCTC 888  
 DB |||||  
 DB 826 CGGTGATGTTGATCAGCGAAGTTGTCTATAAGGGGGCCATATCATCTTAAGCC 885  
 QY 889 AATACTAGGAGAACTCATCAAACTCCTCTCTCTGCAATCCTCATCTCAATTTCCA 948  
 DB |||||  
 DB 886 AGCTTAATAGGAGTTAGTGTGGTGCAGTTCCTTCGAACAGGCTGAAGACGATG 945  
 QY 949 TCAGAACTGAAATCCAGATCAATCCTATGCCACACATGGAAG-----TGGACAAA 999  
 DB |||||  
 DB 946 ATGGTGGCGAGCTGCTGATGATAAATCTTCCAATCTCTTAGCAACCTTGCTTAATCC 1005  
 QY 1000 TGGATTCAGTGCACCCAGAGAAATCAATCAATCAATTCAGATGATGATTTTGAGC 1059  
 DB |||||  
 DB 1006 TAAATTCGCTGCGATGTTGAGCCCTGTTCCAGTTCCTAGTGTAGTATGATGATG 1065  
 QY 1060 AGAGTTCCCAAAAGTCTAAATCAGGAGGAGTGAATATGATGAAGATGAACCTGATGCC 1119  
 DB |||||  
 DB 1066 CTGAGGTGAAGACCCCTACCTGGGGATGATGCTACAGAGGAGGATTTA---GAGTCGA 1122  
 QY 1120 AAGATGGAATTTGAAGGTGAAATAGAGGTTATGTGAGCCCTGGAAGTGAACAGTGA 1179  
 DB |||||  
 DB 1123 AACGCAGGAAATGAGTCTGAGGTTATTGAT---GCTGCTCTGATGGGTAAACCTAA 1179  
 QY 1180 GAGAACTAGATTTAGTTCAGAACCAACCATGATGATATCTCTGATGATGATGATG 1239  
 DB |||||  
 DB 1180 GTGAGCCCGTGTGTCGTTGAGACTGTAAGTGAAGTTGACATCTTTGGATGATGGGTATC 1239  
 QY 1240 GGTGGAGAAATACGGCGAGAAAGTAGTGAAGGCAATCCAAATCCAAGAGTTACTACA 1299  
 DB |||||  
 DB 1240 GTTGGCGAAATATGACAGAAAGTTGTCAAGAGAAACCCCAATCCACGAGTTACTACA 1299  
 QY 1300 AGTGACACACCCAGGATGTCCAGTGAAGCACTGGAAGAGGCTCATGACCTAA 1359  
 DB |||||

Db 1300 AATGCACAAAGCAGAGATCCCTGTGAGGAAGCATGTTGAGAGAGCATGCGCAGATCCCTA 1359  
Qy 1360 GGGCTGTGATCAAACTTATGAGGGAAGACACAAACCATGATGTTCTCTGCAGC 1411  
Db 1360 ATCAGTGATACACAGGTATGAGGAACATACATGAACTGCTGCTGC 1411

## RESULT 15

ABZ14474  
ID ABZ14474 standard; DNA; 1545 BP.

XX AC ABZ14474;

XX DT 21-JAN-2003 (first entry)

XX DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2279.

XX KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX OS Arabidopsis thaliana.

XX PN WO200216655-A2.

XX PD 28-FEB-2002.

XX PF 24-AUG-2001; 2001WO-US26685.

XX PR 24-AUG-2000; 2000US-227866P.

XX PR 26-JAN-2001; 2001US-264647P.

XX PR 22-JUN-2001; 2001US-300111P.

XX PA (SCRI ) SCRIPPS RES INST.

XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX PI Harper JF, Kreps J, Wang X, Zhu T;

XX DR WPI; 2002-304127/34.

XX PT Identifying a stress condition to which a plant cell has been exposed  
XX PT and producing plants with increased tolerance to these abiotic stresses  
XX PT -

XX PS Claim 144; SEQ ID NO 2279; 577bp + Sequence Listing; English.

XX CC The invention relates to identifying a stress condition to which a plant  
XX CC cell has been exposed, comprising:  
XX CC (a) contacting nucleic acid representative of expressed polynucleotides  
XX CC in the plant cell with an array or probes representative of the plant  
XX CC cell genome; and

XX CC (b) detecting a profile of expressed polynucleotides in the plant cell  
XX CC characteristic of a stress response. The method is useful in the  
XX CC production of transgenic plants, cells and seeds and in producing plants  
XX CC with increased tolerance to abiotic stress. The present invention is that  
XX CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used  
XX CC in methods of the invention.

XX CC Note: The sequence data for this patent is not represented in the printed  
XX CC specification but is based on sequence information supplied to Derwent by  
XX CC the European Patent Office.

XX SQ Sequence 1545 BP; 472 A; 356 C; 365 G; 352 T; 0 other;

Query Match 11.5%; Score 221.4; DB 24; Length 1545;  
Best Local Similarity 59.0%; Pred. No. 1.6e-47;  
Matches 447; Conservative 0; Mismatches 286; Indels 24; Gaps 3;

Qy 679 CCCCAATCTCAGACTTTAAGTAGAAGGTTCAGATGATGGGTACAAATGGAGAAATATG 738  
Db 653 CACAACAGCTCTAAATGTTGACAAACCAAGCTGATGCTATTAATCTGCGAAATATG 712

Qy 739 GCCAAAAACAAGTGAAGGGAAGTGAATCCAAAGAGTTATTACAAATGCCATACCCCA 798  
Db 713 GGCAAAAGCAAGTAAAGGTAGCGAGTTTCCAGGAAGCTATTACAAAGTGTACTAATCCAG 772

Qy 799 ATTGCCCTTCAAAGAAGGTTGAGAGCTCTTTAGATGGACAAATTAATCTGAGATAGTTT 858  
Db 773 GATGCTCTGTCAAGAAGGTTGAGAGCTCTTTGATGGACAAGTAACGGAGATTATCT 832  
Qy 859 ATAGGGTACTCATTAACCATCTTAAGCCTCAAAATACTAGGAGAACTCATCAAACTCCT 918  
Db 833 ACAAAGGTGAGACAAATCATGAACCTCTCTCAAAACACTTAAGCGAGGTAAACAAAGATAACA 892  
Qy 919 CTCTCTTTGCAATCCCTCATTCAA-----ATTCCATCAGAACTGAAT 961  
Db 893 CCGCAATATAATGGGAGTTTCGATAAATAACAATCGCGGAGTTCTGAATTTGGGGCAT 952  
Qy 962 CCCAGATCAATCCTA-----TGGCACAATGGAAGTGGACAATAATGGATTCAGCTGCCACCC 1017  
Db 953 CACAGTTTCAAACTAATAGCTCCAACAAGACTAAGAGAGAGCAACATGAAGCAGTAAGTC 1012  
Qy 1018 CAGAAAACCTCATCAATATCAATTGGAGATGATGATTTTGGAGCAGAGTTCCCAAAAGTGTA 1077  
Db 1013 AAGCTACGACAACAGAGCACTTGTCTGAGGCAAGTGACGGTGAAGAAGTTGGTAATGGAG 1072  
Qy 1078 AATCAGGAGGGGATGAATATGATGAAGATGAACCTGTGATGCCAAAGATGGAAAAATTGAAG 1137  
Db 1073 AAACCTGATGTGAGAGAGAAAGATGAGATGAGCTGTATCCCAAGAGAGAAGTACAGAAG 1132  
Qy 1138 GTGAAAAT---GAGGGTATGTGAGCCCTCTGGAAGTAGAACAGTGAAGAACCTTAGAGTTG 1194  
Db 1133 TTGGATTTTCAGAACCAAGCTCTGCTCTTACATAGAACTGTGACAGAGCCTAGAAATTA 1192  
Qy 1195 TAGTTTCAGACACACAGTGCATGATATCTTGTGATGGCTTATAGGTGGAGAAATACG 1254  
Db 1193 TTGTCCAAACGACGAGTGAAGTTGATCTTCTAGATGATGGATATAGGTGGCGGTAAATATG 1252  
Qy 1255 GGCAGAAAAGTAGTGAAGGGCAATCCAAATCCAAAGGAGTTACTACAAGTGCACACACCCAG 1314  
Db 1253 GACAGAAAAGTTGTCAAAGGGAATCTTATCCGAGGAGCTACTACAAGTGCACACACCCAG 1312  
Qy 1315 GATGTCCAGTGAAGGAGCAACGTGGAAAGAGCTCTCATGACCTAAGGCGCTGTGATCACAA 1374  
Db 1313 GATGTGGTGTGAGGAAACATGTGAGAGAGAGCAGCAACAGATCCAAAAGCTGTAGTAACAA 1372  
Qy 1375 CTTATGAGGGGAAGCACAACCAATGATGTTCTCGCAGC 1411  
Db 1373 CATATGAAGGAAACATAAACCATGACCTTCCGCTGC 1409

Search completed: January 20, 2004, 16:25:53

Job time : 538 secs

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 20, 2004, 16:14:38 ; Search time 121 Seconds  
(without alignments)  
7032.948 Million cell updates/sec

Title: US-09-890-811B-9  
Perfect score: 1928  
Sequence: 1 gcacgagtcctgcgcctct.....tcaaaaaaaaaaaaaaaaaa 1928

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	141.6	7.3	306	US-09-313-294A-4059	Sequence 4059, Ap
2	80.6	4.2	7218	US-08-232-463-14	Sequence 14, Appl
3	72.2	3.7	7218	US-08-232-463-14	Sequence 14, Appl
4	52.6	2.7	289	US-09-007-005-17	Sequence 17, Appl
5	52.6	2.7	289	US-09-244-796-17	Sequence 17, Appl
6	45	2.3	1105	US-09-072-596-329	Sequence 329, App
7	43.8	2.3	1893	US-09-328-352-112	Sequence 112, App
8	40.6	2.1	1664976	US-08-916-421B-1	Sequence 1, Appli
9	39	2.0	51259	US-08-781-891-209	Sequence 209, App
10	39	2.0	51259	US-09-618-166-209	Sequence 209, App
11	39	2.0	1664976	US-08-916-421B-1	Sequence 1, Appli
12	38.6	2.0	275	US-08-585-593A-42	Sequence 42, Appl
13	38.6	2.0	16442	US-08-781-891-208	Sequence 208, App
14	38.6	2.0	16442	US-09-618-166-208	Sequence 208, App
15	38	2.0	546	US-09-134-001C-55	Sequence 55, Appl
16	38	2.0	1230	US-09-461-325-80	Sequence 80, Appl
17	37.6	2.0	1926	US-09-249-585A-2	Sequence 2, Appli
18	37.6	2.0	1926	US-09-410-399-3	Sequence 3, Appli
19	37.6	2.0	2580	US-09-050-863-2	Sequence 2, Appli
20	37.6	2.0	2580	US-09-359-081-2	Sequence 2, Appli
21	37.6	2.0	5452	US-09-130-114-1	Sequence 1, Appli
22	37.6	2.0	8705	US-09-647-344A-14	Sequence 14, Appl
23	37.6	2.0	9600	US-08-910-647-1	Sequence 1, Appli
24	37.6	2.0	9600	US-09-620-925-1	Sequence 1, Appli
25	37.6	2.0	10596	US-07-884-811-15	Sequence 15, Appl
26	37.6	2.0	10596	US-07-885-971-15	Sequence 15, Appl
27	37.6	2.0	10596	US-08-087-783A-15	Sequence 15, Appl

c 28	37.6	2.0	10596	1	US-08-194-088B-15	Sequence 15, Appl
c 29	37.6	2.0	10596	2	US-08-194-087-15	Sequence 15, Appl
c 30	37.6	2.0	10596	5	PCT-US93-04648-15	Sequence 15, Appl
c 31	37.2	1.9	1656	3	US-09-072-384-14	Sequence 14, Appl
c 32	37.2	1.9	1679	3	US-09-072-384-17	Sequence 17, Appl
c 33	36.6	1.9	248	3	US-09-007-005-32	Sequence 32, Appl
c 34	36.6	1.9	248	3	US-09-244-796-32	Sequence 32, Appl
c 35	36.6	1.9	277	3	US-09-007-005-3	Sequence 3, Appli
c 36	36.6	1.9	277	3	US-09-244-796-3	Sequence 3, Appli
c 37	36.6	1.9	12752	2	US-08-459-146-1	Sequence 1, Appli
c 38	36.6	1.9	12752	2	US-08-459-065-1	Sequence 1, Appli
c 39	36.4	1.9	2007	3	US-08-747-221B-36	Sequence 36, Appl
c 40	36.4	1.9	2007	3	US-08-747-221B-36	Sequence 38, Appl
c 41	36.4	1.9	2007	3	US-09-005-051-38	Sequence 36, Appl
c 42	36.4	1.9	2007	3	US-09-005-051-38	Sequence 38, Appl
c 43	36.2	1.9	1522	4	US-09-615-192A-371	Sequence 371, App
c 44	36.2	1.9	1830121	4	US-09-557-884-1	Sequence 1, Appli
c 45	36.2	1.9	1830121	4	US-09-643-990A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-09-313-294A-4059  
; Sequence 4059, Application US/09313294A  
; Patent No. 6476212  
; GENERAL INFORMATION:  
; APPLICANT: Lalgudi, Raghunath V.  
; APPLICANT: Ito, Laura Y.  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
; FILE REFERENCE: PL-0017 US  
; CURRENT APPLICATION NUMBER: US/09/313,294A  
; CURRENT FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 7600  
; SOFTWARE: PERL Program  
; SEQ ID NO 4059  
; LENGTH: 306  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6476212 700347613H1  
US-09-313-294A-4059

Query Match	7.3%	Score 141.6;	DB 4;	Length 306;
Best Local Similarity	77.1%	Pred. No. 2.3e-29;		
Matches 185;	Conservative	0;	Mismatches 54;	Indels 1;
Gaps	1;			
QY	1168	GTAGAACAGTGAAGAACCTGAGTTGTAGTTTCAGACCAACCACTGACATTGATATCTTGG	1227	
Db	35	GTAAACCAATCGTAGCCCTGTTGTTGTACAACTGTTAGTAGTTGATATCTTGG	94	
QY	1228	ATGATGGCTATAGTGGAGAAATACGGGCAGAAAGTAGTGAAGGGCAATCCAAATCCAA	1287	
Db	95	ACGATGGGTATCGTTGGGCCAAATATATGGCAGAAAGTAGTGAAGGAAATCCCAACCCAC	154	
QY	1288	GGAGTTACTACAAGTGCACACACCCAGGATGTCAGTAGGAGACGCTGGGAAGAGCCT	1347	
Db	155	GGAGTTACTACAAGTGCACAAATACAGGATGCCCGTCCAGGAAGCATGTTGAGAGACAT	214	
QY	1348	CACATGACCTAAGGGCTGTGATCACAACTATGAGGGAAGCAGCAACCATGATGTTCTCTG	1407	
Db	215	CACATGACCCGA-ATCGGTGATCACACATATGAGGAAACATACCATGATGATGCTCTG	273	

RESULT 2  
US-08-232-463-14  
; Sequence 14, Application US/08232463  
; Patent No. 5670367  
; GENERAL INFORMATION:  
; APPLICANT: DORNER, F.

APPLICANT: SCHEIFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZgpt-F1s  
US-08-232-463-14

Query Match 4.2%; Score 80.6; DB 1; Length 7218;

Best Local Similarity 4.3%; Pred. No. 6.4e-12;

Matches 14; Conservative 213; Mismatches 102; Indels 0; Gaps 0;

QY 8 TCTCATGGCATCTTCTCTGTAGTTTACACACCTCTGCAAGTGCAAACTCTTCACCAA 67  
Db 1126 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1185  
QY 68 CTTACCTCTCCACACACCTTTCATGACACTTCTTCTGACCTCTTGTCTCTC 127  
Db 1186 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1245  
QY 128 CTTGGACACACACAGCACACAGGCTGTCTCTGAGAGACTGGCTCTGTGTTC 187  
Db 1246 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1305  
QY 188 CAAATCAAGTCCACACACACCTCTCTGCTCTCTCTCCCTCCCTCTCTCTC 247  
Db 1306 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1365  
QY 248 TTTCTACTTTGCTATCTCTCTGTTTGGCCCTGCTGAGCTTCTTGAAGTTCGCGGTCT 307  
Db 1366 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1425  
QY 308 CCTTAACCTCTCCACACTTTCACATCTC 336  
Db 1426 YYYYYYYYGTACCAAAATCTTCTATCTC 1454

RESULT 3

US-08-232-463-14/c  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZgpt-F1s  
US-08-232-463-14

Query Match 3.7%; Score 72.2; DB 1; Length 7218;

Best Local Similarity 4.3%; Pred. No. 1.3e-09;

Matches 17; Conservative 235; Mismatches 143; Indels 0; Gaps 0;

QY 1018 CAGAAACTCATCAATPACAAATTTGGAGATGATGATTTGAGCAGAGTTCCCAAAAGTGA 1077  
Db 1435 CRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1376  
QY 1078 AATCAGAGGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1137  
Db 1375 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1316  
QY 1138 GTGAAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1197  
Db 1315 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1256  
QY 1198 TTCAGACACACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1257  
Db 1255 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1196  
QY 1258 AGAAGTAGTAGGAGCAATCCAAATCCAAAGGAGTTACTACAAGTGCACACCCAGGAT 1317  
Db 1195 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1136  
QY 1318 GTCCAGTGAGGAGCACGCTGGAAGAGCCTCATGACCTAAGGGCTGTGATCACAACCT 1377

```

TUBERCULOSIS
METHODS OF DIAGNOSIS OF COMPOUNDS AND
TITLE OF INVENTION: 350
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:

```

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/072,596  
FILING DATE: 05-MAY-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.417C9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 329:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1105 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
US-09-072-596-329

Query Match 2.3%; Score 45; DB 4; Length 1105;  
Best Local Similarity 42.4%; Pred. No. 0.014;  
Matches 108; Conservative 20; Mismatches 127; Indels 0; Gaps 0;  
QY 1305 ACACACCCAGGATGTCAGTGAGGAGCAGCTGGAAAGACCTCACATGACCTAAGGGCT 1364  
DB 156 ACVTRACCCGCCAGYTCAGTGTTRAAACCGGTGTRAGGGCCGACCCAACTAAACGCT 215  
QY 1365 GTGATCAACTTATGAGGAAGACCAACCATGATGTTCTCGAGCCCGTGCAGTGGC 1424  
DB 216 TTAACCAAGRAWTGKTTGGTCCGCCGACCCACCTGTTGTGTGTCCTCTWYCGGTGTAGC 275  
QY 1425 AGCCATTCTGTGAACAGACCAATGCCAAACAAATGCTTCAAACACACCAACACTGCAGCC 1484  
DB 276 GCGGTTTANGCCGGTGGGTYTCAMCASCSCGCGGTATCCCAKCNWTCCTCCCGGCC 335  
QY 1485 ACTTCGGTAAGGCTCTTCCAGTGATCCACCAAGTGACAAATTCCTTTCAGAACCAAGA 1544  
DB 336 MRACCCACCGGCACCTTTRAGCGTGCCGCCAATTCAAAYCKYCTGRWTCCTCTCMAAACA 395  
QY 1545 TCACACGACCAACA 1559  
DB 396 CCACRAAGGCCACM 410

RESULT 7  
US-09-328-352-112  
Sequence 112, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Berton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 112  
LENGTH: 1893  
TYPE: DNA  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-112

Query Match 2.3%; Score 43.8; DB 4; Length 1893;  
Best Local Similarity 57.8%; Pred. No. 0.04; Mismatches 57; Indels 0; Gaps 0;  
Matches 78; Conservative 0;  
QY 1089 GATCAATATGATGAAGATGACCTGATGCCAAAGATGGAATAATTGAAGGTGAAATGAG 1148

Db 235 GATGAAGTTGCTGAAGAAGAAAGCTGCTGCCGTACTGTGTCATCTGTTGAAAATGAGCCTGA 294  
QY 1149 GGTATGTGTCAGCCCTGGAGTAGAAGACAGTGAGAGAACCTAGAGTTGTAGTTTCAGACAAAC 1208  
Db 295 CGTACGACAGACCCCTGACGTATGATGATGCGTGAATGGGTACAGTAGAAGTGTTRACC 354  
QY 1209 ACTGACATTGATATC 1223  
Db 355 CGTGAAGGTGAATC 369  
RESULT 8  
US-08-916-421B-1/c  
Sequence 1, Application US/08916421B  
Patent No. 6503729  
GENERAL INFORMATION:  
APPLICANT: Bult et al.  
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus  
Patent No. 6503729  
FILE REFERENCE: PB275  
CURRENT APPLICATION NUMBER: US/08/916,421B  
CURRENT FILING DATE: 1997-08-22  
PRIOR APPLICATION NUMBER: US 60/024,428  
PRIOR FILING DATE: 1996-08-22  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 1664976  
TYPE: DNA  
ORGANISM: Methanococcus jannaschii  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (28222)..(28222)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (28257)..(28258)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (84773)..(84773)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (84808)..(84808)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (84812)..(84812)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (98120)..(98120)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (98159)..(98159)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (98239)..(98239)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (98266)..(98266)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (98343)..(98343)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (103998)..(103998)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (148948)..(148948)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (163385)..(163385)  
OTHER INFORMATION: n equals a, t, c, or g  
NAME/KEY: misc feature  
LOCATION: (191989)..(191989)





```

; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98120)..(98120)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98159)..(98159)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98239)..(98239)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98266)..(98266)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98343)..(98343)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (103998)..(103998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (148948)..(148948)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (163385)..(163385)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (191989)..(191989)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (191995)..(191995)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (231980)..(231980)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234187)..(234187)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234220)..(234220)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234814)..(234814)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (309398)..(309398)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (309418)..(309418)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (312837)..(312837)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (312993)..(312993)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (319226)..(319226)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559167)..(559167)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559241)..(559241)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (600992)..(600992)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (622708)..(622708)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (657081)..(657081)
; OTHER INFORMATION: n equals a, t, c, or g

```

```

; NAME/KEY: misc feature
; LOCATION: (657203)..(657203)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (674435)..(674435)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (682442)..(682442)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (713652)..(713652)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (741684)..(741684)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (779455)..(779455)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (779676)..(779676)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (855539)..(855539)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (871619)..(871619)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1084830)..(1084830)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1096846)..(1096846)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1119881)..(1119881)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1130881)..(1130881)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1310988)..(1310988)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1313224)..(1313224)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1349473)..(1349473)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1349491)..(1349491)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1470091)..(1470091)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1569020)..(1569020)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1602912)..(1602912)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1603734)..(1603734)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1637998)..(1637998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1664854)..(1664854)
; OTHER INFORMATION: n equals a, t, c, or g

```

US-08-916-421B-1

Query Match 2.0%; Score 39; DB 4; Length 1664976;  
 Best Local Similarity 51.6%; Pred. No. 25;







**THIS PAGE BLANK (USPTO)**

## SUMMARIES

## ALIGNMENTS



QY 61 TCACCAACTTCACCTTCTCCACACACCCCTTTCATGACCACTTCTTTCTCTGACCTCCTTG 120  
Db 75 TCACCAACTTCACCTTCTCCACACACCCCTTTCATGACCACTTCTTTCTCTGACCTCCTTG 134  
QY 121 CTTCTCCCTTGGACACACAAAGCCACCAAGGCTGTTGCTGAGAGAACTGGCTCTG 180  
Db 135 CTTCTCCCTTGGACACACAAAGCCACCAAGGCTGTTGCTGAGAGAACTGGCTCTG 194  
QY 181 GTGTTCCCAAAATTCAGTTCACACACCACTTCTCTGCTCTCTCTCCCTCCCATTT 240  
Db 195 GTGTTCCCAAAATTCAGTTCACACACCACTTCTCTGCTCTCTCTCCCTCCCATTT 254  
QY 241 CTCCTTCTCTTACTTTGCTATTCCTCTGCTGTTGAGCCCTGCTGAGCTTCTTGACTCGC 300  
Db 255 CTCCTTCTCTTACTTTGCTATTCCTCTGCTGTTGAGCCCTGCTGAGCTTCTTGACTCGC 314  
QY 301 CGGTTCTCTTACTTCTTCAACATTCGCAATCTCCAACTGGAGCATTTGTTGCT 359  
Db 315 CGGTTCTCTTAAATCTTCCAACTTCTGCCATCTCCAACTGGAGCATTTGTTGCT 373

## RESULT 3

US-09-878-574-4924  
; Sequence 4924, Application US/09878574  
; Patent No. US20020110548A1  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: Thompson, Michael D.  
; APPLICANT: La Rosa, Thomas J.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(15401)B  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: US/09/878,574  
; PRIOR FILING DATE: 1999-06-14  
; NUMBER OF SEQ ID NOS: 15775  
; SEQ ID NO 4924  
; LENGTH: 421  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: LIB3028-001-Q1-B1-C9  
US-09-878-574-4924

Query Match 17.7%; Score 342.2; DB 10; Length 421;  
Best Local Similarity 93.2%; Pred. No. 3.5e-87;  
Matches 372; Conservative 0; Mismatches 18; Indels 9; Gaps 1;  
QY 4 CGAGTCTCATGGCATCTTCTTCTGGTAGTTTAGACACCTCTGCAAGTGCAAACTCCTTCA 63  
Db 23 CGGCTCGAGTGGCATCTTCTTCTGGTAGTTTAGACACCTCTGCAAGTGCAAACTCCTTCA 82  
QY 64 CCAACTTCACCTTCTCCACACACCCCTTTCATGACCACTTCTTCTGACCTCCTTGCTT 123  
Db 83 CCAACTTCACCTTCTCCACACACCCCTTTCATGACCACTTCTTCTGACCTTCTTGCTT 142  
QY 124 CTCCTTGGACACAAAGCCACCA-----GGGTGTTTCTCTGAGAGAACTG 174  
Db 143 CTCCTTGGACACAAAGCCACCA-----GGGTGTTTCTCTGAGAGAACTG 202  
QY 175 GCTCTGGTGTCCCAATTCAGTTCACACACCACTTCTCTGCTCTCTCTCCCTCC 234  
Db 203 GCTCTGGTGTCCCAATTCAGTTCACACACCACTTCTCTGCTCTCTCTCCCTCC 262  
QY 235 CCAATTCCTCTTCTTACTTTGCTATTCCTCTGCTGTTGAGCCCTGCTGAGCTTCTTG 294  
Db 263 CCAATTCCTCTTCTTACTTTTCTATTCCTCTGCTGTTGAGCCCTGCTGAGCTTCTTG 322  
QY 295 ACTCGCGGTCTCTTAACTTCTTCAACATTCGCAATCTCCAACTGGAGCATTTG 354  
Db 323 ACTCACCTGTCTCTTAACTTCTTCAACATTCGCAATCTCCAACTGGAGCATTTG 382  
QY 355 TTGCTCAGAGCTTCAATTTGAGAGAGAGTTCAGGGGGA 393

Db 383 TTGCTCGGAGCTTCAATTTGAGAGAGAGTTCGGGGGGA 421

## RESULT 4

US-09-878-574-1921  
; Sequence 1921, Application US/09878574  
; Patent No. US20020110548A1  
; GENERAL INFORMATION:  
; APPLICANT: Byrum, Joseph R.  
; APPLICANT: Thompson, Michael D.  
; APPLICANT: La Rosa, Thomas J.  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(15401)B  
; CURRENT FILING DATE: 2001-12-21  
; PRIOR APPLICATION NUMBER: US/09/878,574  
; PRIOR FILING DATE: 1999-06-14  
; NUMBER OF SEQ ID NOS: 15775  
; SEQ ID NO 1921  
; LENGTH: 363  
; TYPE: DNA  
; ORGANISM: Glycine max  
; OTHER INFORMATION: Clone ID: LIB3028-031-Q1-B1-C6  
US-09-878-574-1921

Query Match 16.2%; Score 312.6; DB 10; Length 363;  
Best Local Similarity 93.7%; Pred. No. 9.6e-79;  
Matches 340; Conservative 0; Mismatches 14; Indels 9; Gaps 1;  
QY 15 GCATCTTCTTCTGGTAGTTTAGACACCTCTGCAAGTGCAAACTCCTTACCAACTTCACC 74  
Db 1 GCATCTTCTTCTGGTAGTTTAGACACCTCTGCAAGTGCAAACTCCTTACCAACTTCACC 60  
QY 75 TTCTCCACACACCTTTCATGACCACTTCTTCTGACCTCCTTCTGCTTCTCCTTGGAC 134  
Db 61 TTCTCCACACACCTTTCATGACCACTTCTTCTGACCTTCTTCTGCTTCTCCTCCACAG 120  
QY 135 AACAAAGCCACCA-----GGGTGTTTCTCTGAGAGAACTGGCTCTGCTT 185  
Db 121 AACAAAGCCACCA-----GGGTGTTTCTCTGAGAGAACTGGCTCTGCTT 180  
QY 186 CCAAAATTCAGTTCACACACCACTTCTCTGCTCTCTCTCCCTCCCACTTCTCT 245  
Db 181 CCAAAATTCAGTTCACACACCACTTCTCTGCTCTCTCTCTCCCTCCCACTTCTCT 240  
QY 246 TCTTCTTACTTGTGCTATTCCTCTGCTGTTGAGCCCTGCTGAGCTTCTTGACTGCGGTT 305  
Db 241 TCTTCTTACTTGTGCTATTCCTCTGCTGTTGAGCCCTGCTGAGCTTCTTGACTGCGGTT 300  
QY 306 CTCCTTAACTTTCACACATTCCTGCACTCTCCAACTGGAGCATTTCTTCTCAGAGC 365  
Db 301 CTCCTTAACTTTCACACATTCCTGCACTCTCCAACTGGAGCATTTCTTCTCAGAGC 360  
QY 366 TTC 368  
Db 361 TTC 363

## RESULT 5

US-09-938-842A-804  
; Sequence 804, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE REFERENCE: SCRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A

```

/ CURRENT FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: US 60/227,866
/ PRIOR FILING DATE: 2000-08-24
/ PRIOR APPLICATION NUMBER: US 60/264,647
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/300,111
/ PRIOR FILING DATE: 2001-06-22
/ NUMBER OF SEQ ID NOS: 5379
/ SEQ ID NO 804
/ LENGTH: 1539
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
/ US-09-938-842A-804

```

Query Match	15.0%	Score 308.2	DB 10	Length 1539
Best Local Similarity	67.1%	Prod. No. 4.8e-77		
Matches 493	Conservative 0	Mismatches 218	Indels 24	Gaps 3
Qy	710	AGATGATGGGTACAAATTTGGAGGAATATGGCCAAAACAAAGTGAAGGAAAGTGAATAATCC	769	
Db	528	AGAGATGGTTCAATTTGGAGAAAGTACGACAAACACAGGTGAAGGAAGTGAATCC	587	
Qy	770	AAGAAGTTATTTACAAATGCRATACCCCAATTTGCCCTTACAAAGAAAGGTTTGAGAGGTC	829	
Db	588	TCGGAGTTACTATAAGTGTACTTTCCCTAAATTTGCCAACGAAGAAAGTGGAGAGATC	647	
Qy	830	TTTAGATGGCAAAATTAAGTACAGATAGTTTATAGGGTACTCATAAACCATCCTTAAGCCCTCA	889	
Db	648	TTTGGAAAGGTCAGATCAAGAGATTTGTGTATAAAGGAAGCCAAACCATCTCTAAACCTCA	707	
Qy	890	AAATACTAGGAGAAACTCATCAAACTCTCTTCTCTTGGCAATCCCTCATTCAAATTCAT	949	
Db	708	GTCTACTAGAGATCTTCTCGACTTTTTCGACTTTTTCAGCTGTGTACATGCCAG	767	
Qy	950	CAGAACTGAAATCC-----CAGATCAATCCTATGCCACACATGGAAGTGGACA	997	
Db	768	TTTGGATCAATAATCGTCAAGCTTCTCTGATCAGCCTAAATTCCTAAATAGCTTTTCATCA	827	
Qy	998	AATCGATTTAGCTGCCACCCAGAA-----AATCATCAATATCAATTTGGAGATGA	1048	
Db	828	GTCTGATTCCTTTGGGATGCAACAGAGGATAATATCTACTTCTGATTTCTGTTGGTGACGA	887	
Qy	1049	TGATTTTGGAGCAGAGTTCCCAAAAGTGTAAATCAGGAGGGGATGAATATGATGAAGATGA	1108	
Db	888	TGAGTTTCGAACAAGGCTC---ATCGATTGTCAGCAGACAGCAAGAAAGTTGTGGGAGTGA	944	
Qy	1109	ACCTGATGCCAAAGATGGAAAAATTTGAAGGTGAAAATGAGGGTATGTACGCCCTCGAAG	1168	
Db	945	ACCTGGAAGCAAGAGATGGAAAGGGGCAATGNAACAAATGGTCGGAAATGGTGGTGGAG	1004	
Qy	1169	TAGAACAGTGAAGAGAACTAGAGTTGTAGTTTCAGACCAACAGTGCATTTGATATCTTTGA	1228	
Db	1005	CAAGACAGTGAAGAGCCGAGAAATCGTATGTCAGACAAACGAGTGTATGTGATCTTTGA	1064	
Qy	1229	TGATGGCTTATAGGTGGAGAAAATACGGGCAGAAAAGTGTAGTGAAGGGCAATCCAAATCCAAAG	1288	
Db	1065	CGACGGTTACAGATGGAGAAAATACGGCCAGAAAAGTCGTTAAGGGAAACCCCAATCCAAAG	1124	
Qy	1289	GAGTTACTACAAGTGCACACACCCAGGATGTCAGTGAAGGAGACACGTTGGAAAGAGGCTC	1348	
Db	1125	AAGCTTACTACAAGTGCACCAACATCGGTTGTCCAGTGAAGGAAACATGTGGAGAGAGCATC	1184	
Qy	1349	ACATGACCTAAGGGGTGTGATCAACAATTTATGAGGGAAGCACCAACCATGATGTTTCCTGC	1408	
Db	1185	ACACGACATGAGAGCAGTAATCACACCTACGAAGGGGAAACACCAACCATGATGTTTCCTGC	1244	
Qy	1409	AGCCCGTGGCAGTGG	1423	
Db	1245	AGCTCGTGTAGCGG	1259	

RESULT 6  
US-10-278-536-181

Db 1178 CGAGGTTACAGATGGAGAAATACGCCAGAAAGTCGTTAAGGGAAACCCAAATCAAAG 1237  
 QY 1289 GAGTTACTCAAGTCACACACACAGGATGTCAGTGAGGAACACGTCGAAAGAGCCTC 1348  
 Db 1238 AAGCTACTCAAGTCACACACACAGGATGTCAGTGAGGAACACGTCGAAAGAGCCTC 1297  
 QY 1349 ACATGACCTAAGGCTGTGATCAACAATTATAGGGAAGCAACACATGATGTTCTTCG 1408  
 Db 1298 ACACGACATGAGACAGTATCAACAACCTACGAAAGGGAACACACACACGATGTTCTTCG 1357  
 QY 1409 AGCCCGTGGCAGTGG 1423  
 Db 1358 AGTCGTGGTAGCGG 1372

RESULT 7

US-10-278-173-87  
 ; Sequence 87, Application US/10278173  
 ; Publication No. US20030061637A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jiang, Cai-Zhong  
 ; APPLICANT: Broun, Pierre  
 ; APPLICANT: Riechmann, Jose-Luis  
 ; APPLICANT: Pineda, Omaira  
 ; APPLICANT: Zhang, James  
 ; APPLICANT: Yu, Guo-Liang  
 ; APPLICANT: Pilgrim, Marsha  
 ; APPLICANT: Keddle, James  
 ; APPLICANT: Heard, Jacqueline  
 ; APPLICANT: Reuber, Lynne  
 ; APPLICANT: Ratcliffe, Oliver  
 ; APPLICANT: Adam, Luc  
 ; APPLICANT: Samaha, Raymond  
 ; TITLE OF INVENTION: POLYNUCLEOTIDES FOR ROOT TRAIT ALTERATION  
 ; FILE REFERENCE: MEI-009  
 ; CURRENT APPLICATION NUMBER: US/10/278,173  
 ; PRIOR FILING DATE: 2002-10-21  
 ; PRIOR APPLICATION NUMBER: US/09/533,392  
 ; PRIOR FILING DATE: 2000-03-22  
 ; PRIOR APPLICATION NUMBER: 60/125,814  
 ; PRIOR FILING DATE: 1999-03-23  
 ; NUMBER OF SEQ ID NOS: 177  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 87  
 ; LENGTH: 1398  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; FEATURE:  
 ; OTHER INFORMATION: G177

US-10-278-173-87

Query Match 14.0%; Score 270.6; DB 15; Length 1398;  
 Best Local Similarity 62.5%; Pred. No. 2.7e-66;  
 Matches 473; Conservative 0; Mismatches 254; Indels 30; Gaps 2;  
 QY 683 ACAATCTCAGACTTTAAGTAGAAGGTCCAGATGATGGTACAAATGGAGGAATATGGCCA 742  
 Db 538 ACCAGCATACATGCTGAGTAGGAACTCTAATGATGTTATGTTGGAGAAATACGGTCA 597  
 QY 743 AAAACAAGTGAAGGGAAGTGAATAATCCAGAGATTATTAACAATGCACATACCCCAATTG 802  
 Db 598 GAAACAAGTGAAGGGAAGGGAAGGGAAGGGAAGGGAAGGGAAGGGAAGGGAAGGGAAG 657  
 QY 803 CCTTACAAAGAGAGAGGTTGAGAGGTCCTTAGTAGGACAAATTAAGTATGATGTTATATA 862  
 Db 658 TGTGTTCAAGAGAGATTGTTGAGACGGCTTCTGATGACAGATCCTGATGATCAATTTATA 717  
 QY 863 GGGTACTCAATCAATCCCTAAGCTCAAAATACCTAGGAGAACTCATCAAACTCCTCTTC 922  
 Db 718 AGTGTTGATATATCATCTTAAGCTGAGTTCCCAAGAGA----- 757  
 QY 923 TCTTGCATCCCTCAATTCATTAATTCATGAACTGAAATCCAGATCAATTCCTATGCCAC 982

Db 758 -----CCATCTCAATCTTCATTCACATCATCGGTTAATGGAGGCGCTTGTTTAATCC-- 810  
 QY 983 ACATGGAAGTGCACAAATCGAATTCAGTCCACCCAGAAAACTCATCAATATCAATTCG 1042  
 Db 811 ---TGTCTCTGTTGTAGTGAACCTCATGATCAATCAGAGAACTCTTCGATTCGTTGA 867  
 QY 1043 AGATGATGATTTTGGAGAGAGTTCACAAAAGTGTAAATCAGAGGGGATGAATATGATCA 1102  
 Db 868 CTATAGTATCTTTGAGCAGAAAAAGTTTTAAATCAGAGTATCGTGAGATAGATGAAGAGGA 927  
 QY 1103 AGATGAACCTGATGCCNAAGATGAAATTTCAAGGTGAAATAGGGTATGTCAGCCCC 1162  
 Db 928 GGAACAACCTGAGATGAAGAGGATGAAAGAGAGGATGAAGATGAAGGGATGCTTATAGA 987  
 QY 1163 TGGAAAGTAGAACAGTGAGAGAACCTAGAGTCTAGTTTCAGACAAACAGTGACATTCATAT 1222  
 Db 988 AGTAAGCAAGGAGTTAAGAGCCAGAGTCTGTTTCAGACAAATAGTGATATGATGT 1047  
 QY 1223 CTTGATGATGCTATAGGTGAGAAAAATACGGGAGAAAGTAGTGAAGGGCAATCCAA 1282  
 Db 1048 TCTTATAGATGCTTTAGATGAGGAAATATGTCAAAAAGTTGTCAAAGGAAATACTAA 1107  
 QY 1283 TCCAAAGGATTTACTCAAGTGCCACACACCCAGAGTCTCAGTGAGGAAGCAGTGAAG 1342  
 Db 1108 TCCAAAGGAGTACTACAAGTGCCATTCCAAGGTTGTGAGTGAAGAGCAAGTGAAG 1167  
 QY 1343 AGCCTCACATGACCTAAGGGCTGTGATCACAACCTTATGAGGAAAGCACAACCATGATGT 1402  
 Db 1168 ATCCGACGACGAGAGAGAGAGTCTCTACTACCTATGAGGAAAGACACATCAGATAT 1227  
 QY 1403 TCTGACGCGCTGGCAGTGGCAGCCATTCGTGAAAC 1439  
 Db 1228 CCCAACCGGCTACGCTCGTGAATTTATTGGGAC 1264

RESULT 8

US-09-938-842A-1681  
 ; Sequence 1681, Application US/09938842A  
 ; Patent No. US20020160378A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harper, Jeff  
 ; APPLICANT: Kreps, Joel  
 ; APPLICANT: Wang, Xun  
 ; APPLICANT: Zhu, Tong  
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
 ; TITLE OF INVENTION: SAME, AND METHODS OF USE  
 ; FILE REFERENCE: SCRIPI300-3  
 ; CURRENT APPLICATION NUMBER: US/09/938,842A  
 ; CURRENT FILING DATE: 2001-08-24  
 ; PRIOR APPLICATION NUMBER: US 60/227,866  
 ; PRIOR FILING DATE: 2000-08-24  
 ; PRIOR APPLICATION NUMBER: US 60/264,647  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/300,111  
 ; PRIOR FILING DATE: 2001-06-22  
 ; NUMBER OF SEQ ID NOS: 5379  
 ; SEQ ID NO 1681  
 ; LENGTH: 1182  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; US-09-938-842A-1681

Query Match 14.0%; Score 270.2; DB 10; Length 1182;  
 Best Local Similarity 63.3%; Pred. No. 3.1e-66;  
 Matches 463; Conservative 0; Mismatches 238; Indels 30; Gaps 2;  
 QY 683 ACAATCTCAGACTTTAAGTAGAAGGTCCAGATGATGGTACAAATGGAGGAATATGGCCA 742  
 Db 468 ACCAGCATACATGCTGAGTAGGAACTCTAATGATGTTATGTTGGAGAAATACGGTCA 527  
 QY 743 AAAACAAGTGAAGGGAAGTGAATAATCCAGAGATTATTAACAATGCACATACCCCAATTG 802  
 Db 528 GAAACAAGTGAAGGGAAGGGAAGGGAAGGGAAGGGAAGGGAAGGGAAGGGAAGGGAAG 587

QY 803 CCTACAAAGAGAGGTTGAGAGGCTTTAGATGACAAATTTACTGAGATAGTTTATAA 862  
 Db 588 TGTTTCCAAAGAGAGTTGAGAGGCTTCTGATGACAGATCACTGAGATCATTTATAA 647  
 QY 863 GGGTACTCATACCATCTTAAGGCTCAAAATATCTAGGAGAACTCATCAAACTCTCTTC 922  
 Db 648 AGTGTGTCATATCATCTTAAGGCTGAGTTTCAACCAAGAGA----- 687  
 QY 923 TCTTGAATCCCTCATATCAAAATTCATGAACTGAAATCCCGAGATCAATCTATGCCAC 982  
 Db 688 -----CAATCTCAATCTTCAATACCATCATCGGTTAATGGAGGCGCTTGTAAATCC-- 740  
 QY 983 ACATGNAAGTGGCAAAATGGATTCAGCTGCCACCCAGAAACTCAATATCAATTCG 1042  
 Db 741 ---TGTCTCTGTTAGTGAACCTCATGATCAATCAGAGAACTCTTCGATTTGTTGA 797  
 QY 1043 AGATGATGATTTTGAGCAGAGTTCCCAAAAGTGTAAATCAGAGGGGATGAATATGATGA 1102  
 Db 798 CTATAGTGATCTTGAGCAGAAAGTTTAAATCAGAGTATGGTGAGATAGATGAAGAGA 857  
 QY 1103 AGATGAACCTGATGCCAAAGAGTGAAGAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1162  
 Db 858 GGAACCACTGAGATGAAGAGGATGAAGAGAGGATGAAGAGAGGATGCTATAGA 917  
 QY 1163 TGGAGTGAACAGTGAAGAACTAGAGTTGATGTTTCAACACCAAGTGAATTCATAT 1222  
 Db 918 AGTAAGCAAGAGGATTAAGAGGCAAGAGTTGTTTCAACCAATGAAGTGAATGATGT 977  
 QY 1223 CCTTGATGATGCTATAGTGGAGAAATACGGGCGAGAAAGTGAAGGGCAATCCAA 1282  
 Db 978 TCTTATAGTGGCTTTAGATGGAGAAATATGTCCTCAAGTTGTCAAAGAAATACTAA 1037  
 QY 1283 TCCAAGAGTTACTAAGTGGACACACCAGAGTGTCCAGTGAAGAGCACGTGGAAG 1342  
 Db 1038 TCCAAGAGGCTACTAAGTGGACATTCCTCAAGGTTGTGGAGTGAAGAGCAAGTGAAG 1097  
 QY 1343 AGCTCATGATGCTAAGGCTGTATCAAACTTATGAGGGAAGCACAACTCATGAT 1402  
 Db 1098 ATCCGAGCAGAGAGAGAGGATCTTCACTATGAAAGAGACACAACTCAGATAT 1157  
 QY 1403 TCTGTCAGCCC 1413  
 Db 1158 CCCAACGCCG 1168

RESULT 9  
 US-09-878-574-8719  
 ; Sequence 8719, Application US/09878574  
 ; Patent No. US20020110548A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Byrum, Joseph R.  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Thompson, Michael D.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
 ; TITLE OF INVENTION: Plants  
 ; FILE REFERENCE: 38-21(15401)B  
 ; CURRENT APPLICATION NUMBER: US/09/878,574  
 ; CURRENT FILING DATE: 2001-12-21  
 ; PRIOR APPLICATION NUMBER: 09/333,535  
 ; PRIOR FILING DATE: 1999-06-14  
 ; NUMBER OF SEQ ID NOS: 15775  
 ; SEQ ID NO 8719  
 ; LENGTH: 265  
 ; TYPE: DNA  
 ; ORGANISM: Glycine max  
 ; OTHER INFORMATION: Clone ID: 701101569H1  
 US-09-878-574-8719

Query Match 13.3%; Score 256; DB 10; Length 265;  
 Best Local Similarity 98.1%; Pred. No. 1.3e-62;  
 Matches 259; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 510 ACACAAAGCCATGAGGTTTTCAGAGGCCAGAAACAGGATAATTTTCTCAGAAAG 569  
 Db 2 ACACAAAGCCATGAGGTTTTCAGAGGCCAGAAACAGGATAATTTTCTCAGAAAG 61  
 QY 570 GGTATGATGAACCTGAACCTCTTCTCCATGAGAGTTTTCCTCCCTGAGATTCCTAGT 629  
 Db 62 GGTATGATGAACCTGAACCTCTTCTCCATGAGAGTTTTCCTCCCTGAGATTCCTAGT 121  
 QY 630 GTCCAAACTTAACCATAGCAATGGGTTTCAATCCGATATGGCAATTTACCCCCCAATCT 689  
 Db 122 GTCCAAACTTAACCATAGCAATGGGTTTCAATCCGATATGGCAATTTACCCCCCAATCT 181  
 QY 690 CAGACTTTAAGTAGAAGTGCAGATGATGGGTACAAATGGAGAAATATGGCCAAAACAA 749  
 Db 182 CAGACTTTAAGTAGAAGTGCAGATGATGGGTACAAATGGAGAAATATGGTCAAAACCCA 241  
 QY 750 GTGAAGGGAAGTGAANAATCCAAGA 773  
 Db 242 GTGAAGGGAAGTGAANAATCCAAGA 265

RESULT 10  
 US-10-341-961A-18  
 ; Sequence 18, Application US/10341961A  
 ; Publication No. US20040006787A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Boyce Thompson Institute for Plant Research, Inc.  
 ; APPLICANT: Curagen Corporation  
 ; APPLICANT: Crasta, Oswald  
 ; APPLICANT: Swirsky, Peter  
 ; APPLICANT: Mysore, Kiran  
 ; APPLICANT: Folkerts, Otto  
 ; APPLICANT: Martin, Gregory  
 ; APPLICANT: Ekenren, Sophia  
 ; TITLE OF INVENTION: PLANT DEFENSE-RELATED GENES REGULATED IN RESPONSE TO PLANT-PATHOGE  
 ; FILE REFERENCE: BTI.67A2  
 ; CURRENT APPLICATION NUMBER: US/10/341,961A  
 ; PRIOR FILING DATE: 2003-01-14  
 ; PRIOR APPLICATION NUMBER: 60390249  
 ; PRIOR FILING DATE: 2002-06-20  
 ; PRIOR APPLICATION NUMBER: 60261029  
 ; PRIOR FILING DATE: 2001-01-11  
 ; PRIOR APPLICATION NUMBER: 60348792  
 ; PRIOR FILING DATE: 2002-01-14  
 ; NUMBER OF SEQ ID NOS: 395  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 18  
 ; LENGTH: 496  
 ; TYPE: DNA  
 ; ORGANISM: Lycopersicon esculentum  
 US-10-341-961A-18

Query Match 12.1%; Score 232.8; DB 12; Length 496;  
 Best Local Similarity 71.3%; Pred. No. 8.9e-56;  
 Matches 338; Conservative 0; Mismatches 127; Indels 9; Gaps 2;  
 QY 911 AAATCTCTCTCTTCTTGGCAATCCCTCATTCATAATCCATCAGAACTGAAATCCCATCA 970  
 Db 32 AAGATCATCTTCAATTCAGATTCATAAACCTTGGCTTACTCAACTGGATGTAACAACCA 91  
 QY 971 ATCTATGACACATGGAAGTGGACAAATGGATTCAGCTGCCACCCAGAAATCTCATC 1030  
 Db 92 GCCAAAGCGGTTTCTTGAANAATGGTCAAAGAGACTCTTTGCTGTGTACAGCAATCTTC 151  
 QY 1031 AATATCAATGGAGATGATGATTTTGAAGCAGAGTTCCTCCAAAAGTGTAAATCAGAGGGA 1090  
 Db 152 AGCTTCTTTTGGAGATGAGGATGTTGATCAAGGCTCTCTCTATCAGTAAATCAGGA----- 206  
 QY 1091 TGAATATGATGAGATGAACCTGATGCCAAAGATGAAATTTGAAGGTGAAATGAGGG 1150  
 Db 207 -GAAATGATGAAATGAAACCCCGGCAAGAGATGGAAGGTGACATGGAATGAAACGAGGT 265



QY 1151 TATGTCAGCCCTGGAGTAGAACAAGTACAGTACAGAGAACTAGAGTTGTAGTTTACAGAACACCAAG 1210  
 Db 266 TATATCA---TCTGCAAGTAGAACAAGTACAGTACAGTAACTAGTATCGTAGTTTCAAAACCAAG 322  
 QY 1211 TGACATTGATATCCTTGTATGATGGCTATAGGTGGAGAAATACGGCAGAAAGTACTGAA 1270  
 Db 323 TGACATTGATATACCTTGTATGATGGCTATAGGTGGAGAAATACGGTCAAAAGTGTCTCAA 382  
 QY 1271 GGGCAATCCAAATCCAAAGAGTTACTTACAAAGTGCACACCCAGGATGTCCAGTGAAGAA 1330  
 Db 383 AGGAATCCAAACCCAGAGTTACTTACAAAGTGCACATTTACTGGATGTCCGGTTAGAA 442  
 QY 1331 GCACGTGGAAGAGCTTCAATGACCTAAGAGGCTGTGATCAACAACCTATGAGGG 1384  
 Db 443 GCATGTGGAACGAGCATCTCATGATCTAAGAGCGGTTATCAACAACCTATGAGG 496

RESULT 11  
 US-09-810-264-23  
 ; Sequence 23, Application US/09810264  
 ; Patent No. US2002007675A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Crane, Virginia C.  
 ; APPLICANT: Famodu, Omolayo O.  
 ; APPLICANT: Hu, Xu  
 ; APPLICANT: Lu, Guihua  
 ; APPLICANT: Zhang, Lingyu  
 ; TITLE OF INVENTION: WRKY Transcription Factors and Methods  
 ; FILE REFERENCE: 1183  
 ; CURRENT APPLICATION NUMBER: US/09/810, 264  
 ; PRIOR FILING DATE: 2001-03-16  
 ; PRIOR APPLICATION NUMBER: US 60/190,467  
 ; PRIOR FILING DATE: 2000-03-17  
 ; NUMBER OF SEQ ID NOS: 43  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 23  
 ; LENGTH: 2343  
 ; TYPE: DNA  
 ; ORGANISM: Glycine max  
 US-09-810-264-23

Query Match 12.1%; Score 232.8; DB 9; Length 2343;  
 Best Local Similarity 59.5%; Pred. No. 2.6e-55;  
 Matches 437; Conservative 0; Mismatches 282; Indels 15; Gaps 2;

QY 703 GAAGTTCAGATGATGGGTACAAATGGAGAAATATGCGCCAAACAAAGTGAAGGAGTG 762  
 Db 867 GAGTATCTGATGATGATACAACTGGAGAAATATGCGCCAAACAAATGTTAAAGGAGTG 926  
 QY 763 AAAATCCAAAGAGCTTATTACAAATGCACATACCCCAATTCGCCCTACAAAGAAAGGTTG 822  
 Db 927 AATTTCCAGCAGTATTACAAATGACATCTTAATCTGTGAAGTTAAGAACTATTTG 986  
 QY 823 AGAGGTCTTTAGTAGACAAATTTACTGAGATAGTTTATAAGGGTACTCATACCATCTTA 882  
 Db 987 AACGCTCCCATGATGACAAATCTAGATATATTTACAGGGAACACATGATCATCTTA 1046  
 QY 883 AGCCTCAAAATACTAGAGAACTATCAAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 942  
 Db 1047 AACCTCAACCAACCCCGGTTACTCTGACGAACTATAATGTCTGCAAGAAAGACAGAT 1106  
 QY 943 ATTCCATCAGAACTGAATCCAGATCAATCTCTATGCCACATGGAAGTGGACAATG- 1001  
 Db 1107 CTGATAAGCTTCTTTGACTAGCCGAGATGACAAAGATCCAAATATGTGTGGCCAGGGT 1166  
 QY 1002 -----GATTGAGTGCACCCAGAAACTCATCAATPATCAATTTGGAGATGATG 1050  
 Db 1167 CTCACCTGGCTGAGCCGAGGTTAAACAGAGTTATTGCTGTAGCAACAATGATGGTG 1226  
 QY 1051 ATTTGAGCAGAGTTCCCAAAAGTGTAAATCAGAGGGGATGAATATGATGAAGTGAAC 1110  
 Db 1227 ATCTAGATGTTTGGGGGTTTGTCAACCGGAAATATGATGAGTGGTTGATGATGATC 1286

QY 1111 CTGATGCCAAAGAGATGGAATTTGAAGGTGAAATATGAGGGTATGTGAGCCCTCGGAAGTA 1170  
 Db 1287 CTTCTCTCAAGCGGAAGAAATATGAGCGTTTGGAAATTTGCTGACAT---CACTCTCTGATTTA 1343  
 QY 1171 GAACAGTGAAGAACCTAGAGTTGTAGTTTCAGACAAACAGTGCACATTGATATCTTGTATG 1230  
 Db 1344 ACCTTATCCGGGAGCCACGTTGTTGTACAAACTCTGAGTGAAGTTGATATCTTGGATG 1403  
 QY 1231 ATGGCTATAGGTGGAGAAATACGGGCAGAAATAGTAGTGAAGGCAATCCAAATCCAAAGTA 1290  
 Db 1404 ATGGCTATCTGCTGGCGCAAGTATGGCGAAGGTGTGAGGCAATCTTAACCTTAGTA 1463  
 QY 1291 GTTACTCAAAAGTGCACACCCAGGATGTCCAGTGAAGGACACGTTGGAAGAGGCGCTCAC 1350  
 Db 1464 GTTATTACAAATGCAGAACACCGGTTGCCCGGTTAGAAAAACACGTTGAGAGGCGCATCTC 1523  
 QY 1351 ATGACCTAAGGCTGTGATCAACAATTTATGAGGGAAGACAAACCATGATGTTCTTGCAAG 1410  
 Db 1524 ATGATCCAAAGCTGTGATTTACAGTATGAGGGGAAACACAATCATGATGTACCAACTG 1583  
 QY 1411 CCCGTGGCAGTGGC 1424  
 Db 1584 CAAGGAATAGTTGC 1597

RESULT 12  
 US-10-341-961A-156  
 ; Sequence 156, Application US/10341961A  
 ; Publication No. US20040006787A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Boyce Thompson Institute for Plant Research, Inc.  
 ; APPLICANT: Curagen Corporation  
 ; APPLICANT: Crasta, Oswald  
 ; APPLICANT: Swirsky, Peter  
 ; APPLICANT: Mysore, Kiran  
 ; APPLICANT: Folkerts, Otto  
 ; APPLICANT: Martin, Gregory  
 ; APPLICANT: Ekengren, Sophia  
 ; TITLE OF INVENTION: PLANT DEFENSE-RELATED GENES REGULATED IN RESPONSE TO PLANT-PATHOGE  
 ; FILE REFERENCE: BTI.67A2  
 ; CURRENT APPLICATION NUMBER: US/10/341,961A  
 ; CURRENT FILING DATE: 2003-01-14  
 ; PRIOR APPLICATION NUMBER: 60390249  
 ; PRIOR FILING DATE: 2002-06-20  
 ; PRIOR APPLICATION NUMBER: 60261029  
 ; PRIOR FILING DATE: 2001-01-11  
 ; PRIOR APPLICATION NUMBER: 60348792  
 ; PRIOR FILING DATE: 2002-01-14  
 ; NUMBER OF SEQ ID NOS: 395  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 156  
 ; LENGTH: 574  
 ; TYPE: DNA  
 ; ORGANISM: Lycopersicon esculentum  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (530)..(530)  
 ; OTHER INFORMATION: Unknown nucleotide 530  
 US-10-341-961A-156

Query Match 11.9%; Score 229.2; DB 12; Length 574;  
 Best Local Similarity 68.4%; Pred. No. 1.1e-54;  
 Matches 347; Conservative 0; Mismatches 154; Indels 6; Gaps 2;

QY 638 TAACCATGACATGGGTTTCAATCCGATTATCGCAATTACCCCCCACCAATCTCAGACTTT 697  
 Db 71 TATGCAAGATATATGATCAGAACAAATAGTGTGAAACCAATACATACAGATATAAGGA 130  
 QY 698 AAGTGAAGGTGAGATGATGGGTACAAATTTGAGGAAATATGCGCAAAACAAAGTGAAGG 757  
 Db 131 GCAGAAAAGGTGAGATGACGGGATCAAAATTTGGAGGAAATACTGCTGAAAACAAAGTAAAG 190

758	QY	AACTGAAATCCCAAGAAGTTATTACAAATGCATACCCCAATTGCCTTACAAAGAAGAA	817
191	Db	TATGTGAAATCCGAGAAAGCTACTCAAGTGTACATACCCCAATTGTCCCAACCATGAAGAA	250
818	QY	GGTTGAGAGGCTCTTTAGATGGCAAAATTACTGAGATAGTTTATAAGGGTACTCATAAACCA	877
251	Db	GGTTGAGAGATCTTTAGATGGTCAAAATTACTGAAATTGTGACAAATGGTAAATCACAACCA	310
878	QY	TCCTAAGCCTCAAAATACTAGAGGAAACTCATCAAACTCCTCTCTCTTTCGAAATCCCTCA	937
311	Db	TCCAAAGCCTCAGTCTACCAGAAAGATGGTCATCATCCACAGCTTTCATCTGCATTTCCAATC	370
938	QY	TTCAAATTTCCATCAGAACTGAAATCCAGATCAATCCTATGCCACACATGGAAAGTGGACA	997
371	Db	TTTCAATACACAACAACTAAATGAAATTCAGATCA---TCAAATCTATGGTTTCAAATGGACA	427
998	QY	AATGGATTACAGCTGCCACCCACAGAAACTCATCAATATCAATTTGGAGATGATGATTTTGA	1057
428	Db	AATGGATTCCGGTTGCAACACACTGAGAAATTTCTTCGATTTCAATTTGGGGATGATGATCATGA	487
1058	QY	GCAGAGTTCCCAAAAG---TGTAATCAGAGGGGGATGAATATGATGAAGATGAACCTGA	1114
488	Db	ACACACTTGTCAAAAGAGTAGTAGGTCAAGAAGAGATGATCTNGATGAAGAGGAACCCAGA	547
1115	QY	TGCCAAAGATGGAAATTTGAAGGTGA	1141
548	Db	CTCATTAAGATGGAAAGAGAAACCA	574

RESULT 13  
 US-09-938-842A-425  
 ; Sequence 425, Application US/09938842A  
 ; Patent No. US20020160378A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harper, Jeff  
 ; APPLICANT: Kreps, Joel  
 ; APPLICANT: Wang, Xun  
 ; APPLICANT: Zhu, Tong  
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
 ; TITLE OF INVENTION: SAME, AND METHODS OF USE  
 ; FILE REFERENCE: SCRIPI300-3  
 ; CURRENT APPLICATION NUMBER: US/09/938,842A  
 ; CURRENT FILING DATE: 2001-08-24  
 ; PRIOR APPLICATION NUMBER: US 60/227,866  
 ; PRIOR FILING DATE: 2000-08-24  
 ; PRIOR APPLICATION NUMBER: US 60/264,647  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/300,111  
 ; PRIOR FILING DATE: 2001-06-22  
 ; NUMBER OF SEQ ID NOS: 5379  
 ; SEQ ID NO 425  
 ; LENGTH: 1542  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 US-09-938-842A-425

862	AGGGTACTCATTAACCACTCTTAGCCTCAAAATCTAGGAGAACTCATCAAACTCCTCTT	921
Qy		
899	AGGGTCAACACAAATCATGAGCTTCTCAAAGCGGTAAACAATAACGGAGGTGTAAAA	958
Db		
922	CTCTTGCATCCCTCATTCAAATCCATCAGAACTCCAGATCAATCCTATGCCA	981
Qy		
959	GTTCTGATATTGCAATCATAGTTTCAACCAAGTAATAGCAGTCTCAACAGAGTAAGGG	1018
Db		
982	CACATGGAAGTGACAAATCGATTCAGCTGCCACCCAGAAAACTCATCAATATCAATTG	1041
Qy		
1019	ACCGAGAAACAACCA-----AGTTACAACACAGACAGATGCTGAAAGCAAGTG	1069
Db		
1042	GAGATGATGATTTGACAGAGTTCCCAAAAGTGTTAAATCAGGAGGGATGAATATGATG	1101
Qy		
1070	ATAGCGAGGAGGTTGG-----AATCGACAGACTAGTGTGGGAGAAAGACATG	1117
Db		
1102	AGATGAACTGATGTCAAAAGATGGAATTTGAAGTGAATAATGAGGGTATGTCAGCCC	1161
Qy		
1118	AGGATGAGCTGATCCCAAGCGAAGAATAACAGAGTTCGGGTTTCAGAACCAAGTTGCTT	1177
Db		
1162	CTGGAAGTAGAACAGTGCAGAGAACCTTAGAGTTGTAGTTCAGACAAACAGTGCATGATA	1221
Qy		
1178	CATCGCATAGAACTGTGCAGAGCCTAGGATTATTGTTCCAAACGACGAGTGAAGTTGACC	1237
Db		
1222	TCCTTGATGATGCTATAGTGGAGAAAAATACGGGCAGAAAAAGTAGTGAAGGGCAATCCAA	1281
Qy		
1238	TCTTAGATGATGATATAGTGGCGCAAGTATGCTCAGAAAAGTAGTCAAAAGGAAATCCCTT	1297
Db		
1282	ATCCAGGAGTTACTACAGTGCACACCCAGGATGTCAGTGAGGAGACAGTGGAAA	1341
Qy		
1298	ATCCGAGGAGCTACTATAAGTGTACAAACCAAGTTGCGGAGTAGGAAACATGTTAGAGA	1357
Db		
1342	GAGCCTCACATGACCTTAAGGGCTGTGATCACACTTATGAGGGAAGAACCAACCATGATG	1401
Qy		
1358	GACAGCACTGACCCAAAGCTGTTGTAAACAACATATGAAGGTAAACATAACCATGATG	1417
Db		
1402	TTCTCGAGCCCGTGGCAGTGGAGGCATT	1431
Qy		
1418	TTCCAGCTGCTGAAGCAACGAGCAGGCATCAGT	1447
Db		

```

1 RESULT 14
2 US-10-295-403-77
3 ; Sequence 77, Application US/102955403
4 ; Publication No. US20030101481A1
5 ; GENERAL INFORMATION:
6 ; APPLICANT: Heard, Jacqueline
7 ; APPLICANT: Riechmann, Jose Luis
8 ; APPLICANT: Adam, Luc
9 ; APPLICANT: Broun, Pierre
10 ; APPLICANT: Pineda, Omaira
11 ; APPLICANT: Reuber, Lynne
12 ; APPLICANT: Jiang, Cai-Zhong
13 ; APPLICANT: Keddle, James
14 ; APPLICANT: Zhang, James
15 ; APPLICANT: Benito, Maria-Ines
16 ; APPLICANT: Yu, Guo-Liang
17 ; APPLICANT: Fromm, Mike
18 ; TITLE OF INVENTION: PLANT GENE SEQUENCES I
19 ; FILE REFERENCE: MBI-0003
20 ; CURRENT APPLICATION NUMBER: US/10/295,403
21 ; CURRENT FILING DATE: 2002-11-15
22 ; PRIOR APPLICATION NUMBER: US/09/394,519
23 ; PRIOR FILING DATE: 1999-09-13
24 ; PRIOR APPLICATION NUMBER: 60/101,349
25 ; PRIOR FILING DATE: 1998-09-22
26 ; PRIOR APPLICATION NUMBER: 60/103,312
27 ; PRIOR FILING DATE: 1998-10-06
28 ; PRIOR APPLICATION NUMBER: 60/108,734
29 ; PRIOR FILING DATE: 1998-11-17
30 ; PRIOR APPLICATION NUMBER: 60/113,409
31 ; PRIOR FILING DATE: 1998-12-22
32 ; NUMBER OF SEQ ID NOS: 170

```

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 77  
LENGTH: 2044  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (197)..(1735)  
OTHER INFORMATION: G878  
OTHER INFORMATION: "n" at various positions throughout the sequence  
OTHER INFORMATION: may be A, T, C, G, other or unknown  
US-10-295-403-77

Query Match 11.9%; Score 228.8; DB 15; Length 2044;  
Best Local Similarity 58.9%; Pred. No. 3.4e-54;  
Matches 442; Conservative 0; Mismatches 287; Indels 21; Gaps 2;  
QY 682 CACAACTCTAGACTTTAAGTAGAAGGTCAGATGCGGTCAATTTGAGGAAATATGGCC 741  
DB 915 CACAGCCTCAAAATGCTGACAAACCCAGCTGATGATGATACAACTGCGGAAATATGGC 974  
QY 742 AAAACAAGTGAAGGGAAGTGAATCCAAAGAGTTATTACAAATGCACATACCCCAATT 801  
DB 975 AGAAGCAAGTGAAGGAGGAGGATTTCTCGAGTTATTACAAATGTACGCATCCAGCTT 1034  
QY 802 GCCTTACAAAGAAGAGGTTGAGAGGTTCTTTAGATGACAAATTTACTTGAGATAGTTTATA 861  
DB 1035 GTCTGTCAAGAGAAGTGAAGGTCAGTCTCGATGGACAAGTAAACGGAATCATCTACA 1094  
QY 862 AGGTTACTATACCATCTTAAGCCTCAAAATCTAGGAGAAATCATCAAACTCCTCTT 921  
DB 1095 AGGTTCAACAATCATGAGCTTCTCAAAAGCGCGTTAACTAAACGCGGAGTTGTAATA 1154  
QY 922 CTCTTGCAATCCCTCATTTCAATTTCCATCAGAACTGAAATCCCAGATCAATCCTATGCCA 981  
DB 1155 GTTCTGATATTGCAATTCAGTTTCAAAAGTAATAGCAGTCTCAACAGAGTAAGAGGG 1214  
QY 982 CACATGGAAGTGAACAAATGGATTGAGTCCACCCAGAGAAATCTCATCAATATCAATTG 1041  
DB 1215 ACCAGGAAACAAGCA-----AGTTACACACACAGAGCAGATCTCTGAAGCAAGTG 1265  
QY 1042 GAGATGATGATTTGACGAGAGTTCCTCAAAAGTGTAAATCAGGAGGGAATGAATATGATG 1101  
DB 1266 ATAGCGAGGAGGTTGGG-----AATGACAGAGACTAGTGTGGGAGAAAGACATG 1313  
QY 1102 AAGTGAACCTGATGCCAAAGATGGAATTTGAAGTGAATGAGGTATGTCAGCCC 1161  
DB 1314 AGGATGAGCTGATGCCAAGCGAAGAAATACAGAAAGTTGCGGTTTCAGAACCCAGTTGCTT 1373  
QY 1162 CTGGAAGTAGAACAAGTGAAGAACCTTAGAGTTGTAGTTTCAGACAAACAGTGACATTTGATA 1221  
DB 1374 CATCGCATAGAACTGTGACAGAGCTTAGGATTTATGTTCCAAACGACGAGTGAAGTTGACC 1433  
QY 1222 TCCTTGATGATGCTATAGTGTGAGAAATAACCGGCGAGAAAGTAGTGAAGGGCAATCCAA 1281  
DB 1434 TCTTAGATGATGATATAGTGTGCGCAAGTATGCTCAGAAAGTAGTCAAAAGGAAATCCTT 1493  
QY 1282 ATCCAGGAGTACTACAAAGTGCACACCCAGGATGTCAGTGAAGAACCACTGGAAA 1341  
DB 1494 ATCCAGGAGTACTATAGTGTACACACCCAGATTCGCGAGTAGGAAACATGTAGAGA 1553  
QY 1342 GAGCTTCAATGACCTAAGGCTGTGATCAACTTATGAGGGAAGACCAACCATGATG 1401  
DB 1554 GAGCAGCACTGACCCAAAGAGCTGTTGTACACATATAGAGTAAACATACCATGATG 1613  
QY 1402 TTCCTGAGCCCGTGGCAGTGGCAGCCATT 1431  
DB 1614 TTCAGCTGTAGAACCCAGCAGCCATCAGT 1643

RESULT 15

US-09-938-842A-2279

Sequence 2279s, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:  
APPLICANT: Harper, Jeff  
APPLICANT: Kreps, Joel  
APPLICANT: Wang, Xun  
APPLICANT: Zhu, Tong  
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
FILE REFERENCE: SCRIP1300-3  
CURRENT APPLICATION NUMBER: US/09/938,842A  
CURRENT FILING DATE: 2001-08-24  
PRIOR APPLICATION NUMBER: US 60/227,866  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/264,647  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/300,111  
PRIOR FILING DATE: 2001-06-22  
NUMBER OF SEQ ID NOS: 5379  
SEQ ID NO 2279  
LENGTH: 1545  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-09-938-842A-2279

Query Match 11.5%; Score 221.4; DB 10; Length 1545;  
Best Local Similarity 59.0%; Pred. No. 3.7e-52;  
Matches 447; Conservative 0; Mismatches 286; Indels 24; Gaps 3;  
QY 679 CCCCAATCTCAGACTTTAAGTAGAAGTCAAGTCAATGCGGTACAAATTCGAGGAAATATG 738  
DB 653 CCAACAGCCTCTAAATGTTGCAAAACCCAGCTGATGCGCTATTAATCGCGGAAATATG 712  
QY 739 GCCAAACAAGTGAAGGGAAGTGAATAATCCAAAGAGTTATTACAAATGCACATACCCCA 798  
DB 713 GCGAAAGCAGTTAAGTAGGAGTTTCACGAGCTATTACAGTGTACTTAATCCAG 772  
QY 799 ATTGCCCTCAAGAAGAAGTTGAGAGTCTTTAGATCGACAAATTAATCTGAGATAGTTT 858  
DB 773 GATGCTCTCAAGAAGAAGTTGAGAGATCTCTTGATGCAAGTAAACGAGATATCT 832  
QY 859 ATAAGGTTACTATTAACCATCTTAAGCCTCAAAATCTAGGAGAAATCTCATCAATCCT 918  
DB 833 ACAAAGGTGAGCACAATCATGAACCTCTCTCAAAACACTAAGCGAGGTAAACAAAGATAA 892  
QY 919 CTCTCTTCCATCCCTCATTCAA-----ATTCCATCAGAACTCAAAAT 961  
DB 893 CCGGATTAATAATGGAGTTTGAATAATAACAAATCCGCGGAGTTCTGAATTTGGGGGAT 952  
QY 962 CCCAGATCAATCCTA-----TGCCACACATGGAAGTGGACAAATGGATTTCAGCTGCCACCC 1017  
DB 953 CACAGTTTCAAACTAATAGCTCCAAACAGACTAAGAGAGACCAACATGAAGCAGTAAGTC 1012  
QY 1018 CAGAAACTCATATATCAATTTGAGATGATGATTTTGAAGCAGAGTTCCCAAAAGTGA 1077  
DB 1013 AAGTACGACAAACAGAGCACTTTGCTGAGGCAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1072  
QY 1078 AATCAGGAGGAGTGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1137  
DB 1073 AACTGATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1132  
QY 1138 GTGAAAT---GAGGATATGTGAGGCTTGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1194  
DB 1133 TTCCGATTTCAACACCCAGCTCTGCTTTCATATAGACTGTGACAGAGCTTAGAATTA 1192  
QY 1195 TAGTTTCAGACAAACAGTGCATGATATCTTTGATGATGATGATGATGATGATGATGATGATG 1254  
DB 1193 TTGTCCAAACGAGCAGTGAAGTTGATCTTCTAGATGATGATGATGATGATGATGATGATG 1252  
QY 1255 GCGAGAAAGTGTGAGGAGGCAATCCAAATCCAAAGGAGTTTACTACAGTGCACACACCCAG 1314  
DB 1253 GACAGAAAGTTGTCAAAAGGGAATCCTTTATCCGAGGAGCTACTACAAAGTGCACACACCCAG 1312  
QY 1315 GATGTCCAGTGAGGAGCAGCGTGAAGAGAGCTTCAATGACCTTAAGGGCTGTGATCACA 1374

Db 1313 GATGTGTTGAGGAAACATGTTAGAGAGAGACCAACAGATCCAAAAGCTGTAGTAACAA 1372  
Qy 1375 CTTATGAGGAAAGCAACCATGATGTTCTTCGAGC 1411  
Db 1373 CATATGAAGGAAACATAACCATGACCTTCCCGCTGC 1409

Search completed: January 20, 2004, 21:28:58  
Job time : 649 secs